



wwPDB EM Validation Summary Report ⓘ

Aug 25, 2026 – 04:51 PM EDT

PDB ID : 11IQ / pdb_000011iq
EMDB ID : EMD-75724
Title : Rabbit 80S with eEF2,eIF5A and SERBP1
Authors : Seraj, Z.; Zottig, X.; Huang, C.H.; Loveland, A.B.; Diggs, S.; Sholi, E.; Grigorieff, N.; Korostelev, A.A.
Deposited on : 2026-02-26
Resolution : 2.40 Å(reported)
Based on initial model : 7TOR

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

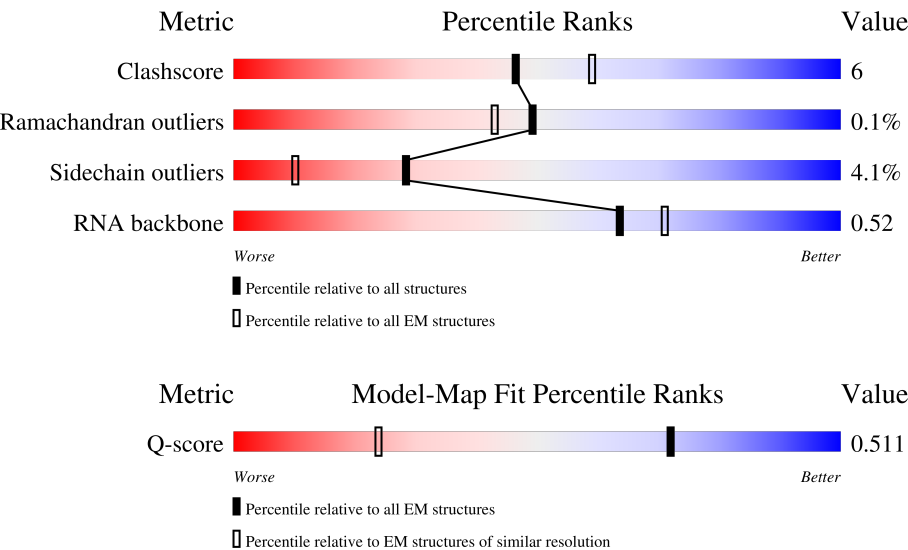
EMDB validation analysis : 0.0.1.dev133
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 2.40 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



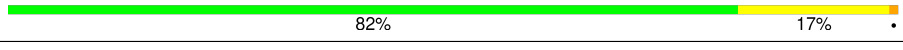
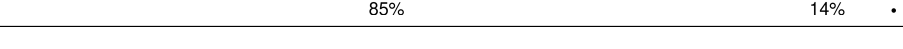
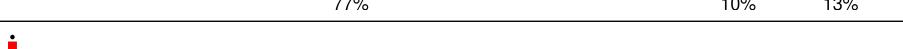
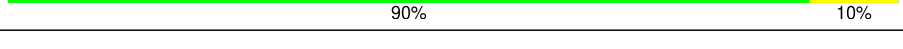
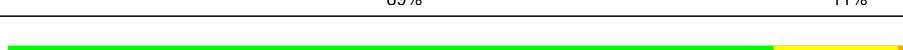
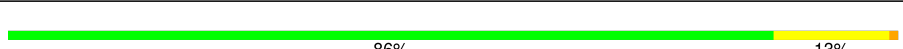
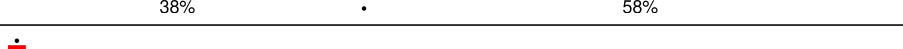
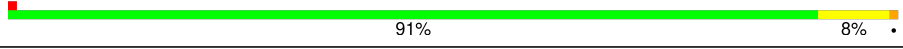
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	5628 (1.90 - 2.90)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	17	183	14% 86% 12% ••
2	DD	151	• 89% 5% 5%
3	58	156	47% 47% ••

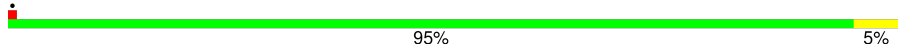
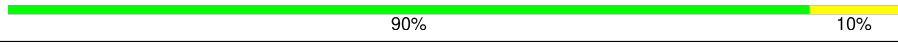
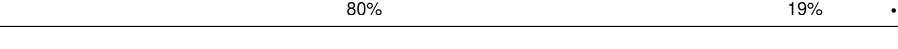
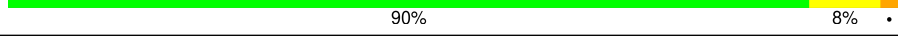
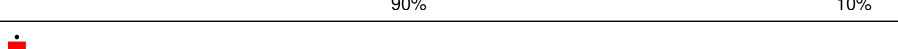
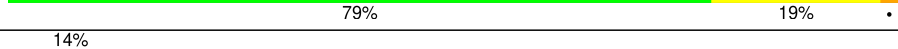
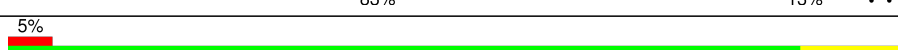
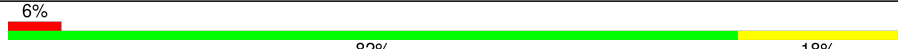
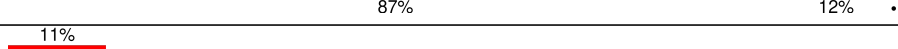
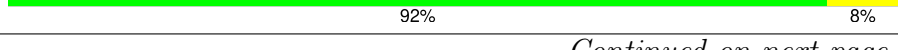
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Mol	Chain	Length	Quality of chain
4	5	120	
5	L8	248	
6	L3	394	
7	L4	362	
8	L5	293	
9	L6	291	
10	L7	253	
11	aa	240	
12	13	241	
13	14	138	
14	15	203	
15	bb	199	
16	20	176	
17	21	159	
18	22	99	
19	cc	118	
20	26	134	
21	27	135	
22	dd	147	
23	29	245	
24	31	107	
25	32	128	
26	ee	109	
27	34	114	
28	35	122	

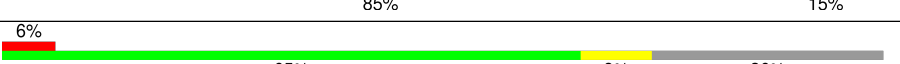
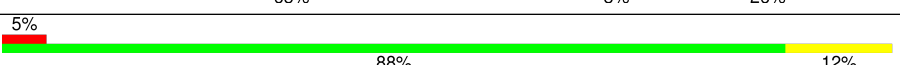
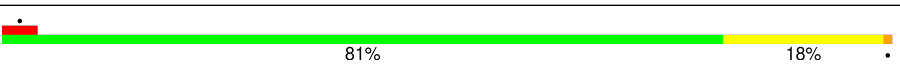
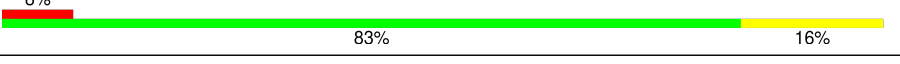
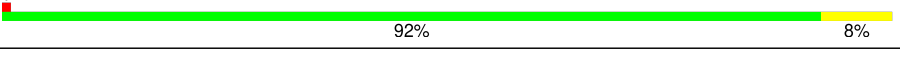
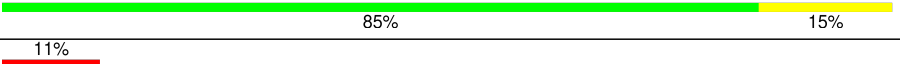
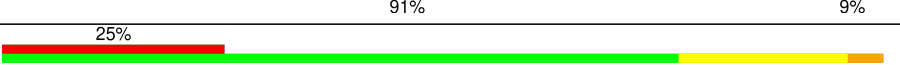
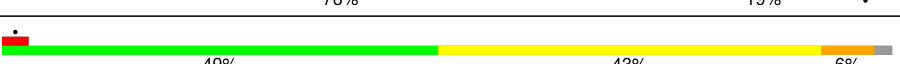
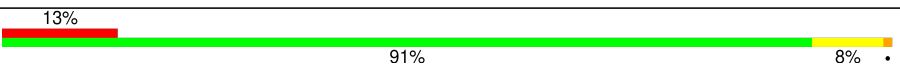
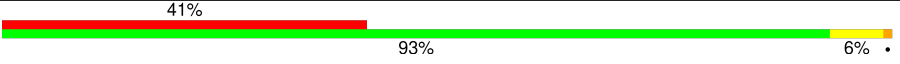
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Mol	Chain	Length	Quality of chain
29	36	102	
30	37	86	
31	38	69	
32	39	50	
33	40	52	
34	41	25	
35	42	104	
36	ff	91	
37	gg	124	
38	s	196	
39	EB	375	
40	Q	188	
41	10	213	
42	L9	190	
43	S7	189	
44	S9	185	
45	S4	262	
46	S6	237	
47	SS	124	
48	RR	141	
49	YY	55	
50	LL	144	
51	11	170	
52	GG	135	
53	23	139	

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Mol	Chain	Length	Quality of chain
54	19	180	
55	v	857	
56	S3	228	
57	FF	149	
58	S8	206	
59	S2	221	
60	BB	295	
61	UU	101	
62	PP	83	
63	JJ	132	
64	AS	213	
65	VV	83	
66	QQ	129	
67	24	157	
68	30	114	
69	ZZ	68	
70	18	1698	
71	MM	141	
72	AA	313	
73	OO	100	
74	RB	407	
75	EE	132	
76	CC	96	
77	II	142	
78	TT	75	

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Mol	Chain	Length	Quality of chain
79	WW	62	
80	XX	55	
81	B	149	
82	u	217	
83	S5	191	
84	A	131	
85	t	153	
86	28	4807	
87	ES	5070	

2 Entry composition

There are 89 unique types of molecules in this entry. The entry contains 224491 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Large ribosomal subunit protein uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	17	183	Total	C	N	O	S	0	0
			1490	935	287	258	10		

- Molecule 2 is a protein called Small ribosomal subunit protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	DD	143	Total	C	N	O	S	0	0
			1175	749	222	198	6		

- Molecule 3 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	58	151	Total	C	N	O	P	0	0
			3208	1432	564	1062	150		

- Molecule 4 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	5	120	Total	C	N	O	P	0	0
			2558	1141	456	842	119		

- Molecule 5 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	L8	248	Total	C	N	O	S	0	0
			1898	1189	389	314	6		

- Molecule 6 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	L3	394	Total	C	N	O	S	0	0
			3172	2020	597	542	13		

- Molecule 7 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	L4	362	Total	C	N	O	S	0	0
			2883	1812	577	480	14		

- Molecule 8 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	L5	293	Total	C	N	O	S	0	0
			2391	1512	438	427	14		

- Molecule 9 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	L6	216	Total	C	N	O	S	0	0
			1729	1115	329	282	3		

- Molecule 10 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	L7	225	Total	C	N	O	S	0	0
			1874	1205	358	302	9		

- Molecule 11 is a protein called Large ribosomal subunit protein eL8.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	aa	233	Total	C	N	O	S	0	0
			1879	1199	361	315	4		

- Molecule 12 is a protein called Large ribosomal subunit protein eL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	13	210	Total	C	N	O	S	0	0
			1701	1065	354	278	4		

- Molecule 13 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	14	138	Total	C	N	O	S	0	0
			1137	727	221	182	7		

- Molecule 14 is a protein called 60S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	15	203	Total	C	N	O	S	0	0
			1701	1072	359	266	4		

- Molecule 15 is a protein called Large ribosomal subunit protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	bb	199	Total	C	N	O	S	0	0
			1630	1051	319	255	5		

- Molecule 16 is a protein called Large ribosomal subunit protein eL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	20	176	Total	C	N	O	S	0	0
			1462	930	285	236	11		

- Molecule 17 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	21	159	Total	C	N	O	S	0	0
			1298	823	252	217	6		

- Molecule 18 is a protein called Large ribosomal subunit protein eL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	22	99	Total	C	N	O	S	0	0
			809	519	141	147	2		

- Molecule 19 is a protein called Large ribosomal subunit protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	cc	118	Total	C	N	O	S	0	0
			967	618	181	167	1		

- Molecule 20 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	26	134	Total	C	N	O	S	0	0
			1115	700	226	186	3		

- Molecule 21 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	27	135	Total	C	N	O	S	0	0
			1107	714	208	182	3		

- Molecule 22 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	dd	147	Total	C	N	O	S	0	0
			1162	734	239	185	4		

- Molecule 23 is a protein called Large ribosomal subunit protein eL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	29	104	Total	C	N	O	S	0	0
			848	527	189	129	3		

- Molecule 24 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	31	107	Total	C	N	O	S	0	0
			888	560	171	155	2		

- Molecule 25 is a protein called Large ribosomal subunit protein eL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	32	128	Total	C	N	O	S	0	0
			1053	667	216	165	5		

- Molecule 26 is a protein called Large ribosomal subunit protein eL33.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	ee	109	Total	C	N	O	S	0	0
			876	555	174	143	4		

- Molecule 27 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	34	114	Total	C	N	O	S	0	0
			906	566	187	147	6		

- Molecule 28 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	35	122	Total	C	N	O	S	0	0
			1013	640	204	168	1		

- Molecule 29 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	36	102	Total	C	N	O	S	0	0
			830	520	176	129	5		

- Molecule 30 is a protein called 60S ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	37	86	Total	C	N	O	S	0	0
			705	434	155	111	5		

- Molecule 31 is a protein called Large ribosomal subunit protein eL38.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	38	69	Total	C	N	O	S	0	0
			569	366	103	99	1		

- Molecule 32 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	39	50	Total	C	N	O	S	0	0
			447	286	96	64	1		

- Molecule 33 is a protein called Large ribosomal subunit protein eL40.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	40	52	Total	C	N	O	S	0	0
			429	266	90	67	6		

- Molecule 34 is a protein called eL41.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	41	25	Total	C	N	O	S	0	0
			239	145	64	27	3		

- Molecule 35 is a protein called eL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	42	104	Total	C	N	O	S	0	0
			851	533	174	138	6		

- Molecule 36 is a protein called 60S ribosomal protein L37a.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	ff	91	Total	C	N	O	S	0	0
			708	445	136	120	7		

- Molecule 37 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	gg	124	Total	C	N	O	S	0	0
			990	615	202	167	6		

- Molecule 38 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	s	196	Total	C	N	O	S	0	0
			1507	959	263	276	9		

- Molecule 39 is a protein called Proliferation-associated protein 2G4.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	EB	375	Total	C	N	O	S	0	0
			2932	1844	509	562	17		

- Molecule 40 is a protein called Large ribosomal subunit protein eL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Q	187	Total	C	N	O	S	0	0
			1514	946	315	249	4		

- Molecule 41 is a protein called Ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	10	209	Total	C	N	O	S	0	0
			1696	1075	328	280	13		

- Molecule 42 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	L9	190	Total	C	N	O	S	0	0
			1516	954	284	272	6		

- Molecule 43 is a protein called Small ribosomal subunit protein eS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	S7	185	Total	C	N	O	S	0	0
			1488	952	271	264	1		

- Molecule 44 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	S9	185	Total	C	N	O	S	0	0
			1525	969	306	248	2		

- Molecule 45 is a protein called 40S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	S4	262	Total	C	N	O	S	0	0
			2076	1324	386	358	8		

- Molecule 46 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	S6	237	Total	C	N	O	S	0	0
			1923	1200	387	329	7		

- Molecule 47 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	SS	124	Total	C	N	O	S	0	0
			1011	640	198	168	5		

- Molecule 48 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	RR	141	Total	C	N	O	S	0	0
			1098	693	219	183	3		

- Molecule 49 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	YY	55	Total	C	N	O	S	0	0
			443	274	97	71	1		

- Molecule 50 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	LL	144	Total	C	N	O	S	0	0
			1190	746	241	202	1		

- Molecule 51 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	11	170	Total	C	N	O	S	0	0
			1362	861	254	241	6		

- Molecule 52 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	GG	135	Total	C	N	O	S	0	0
			1007	615	198	188	6		

- Molecule 53 is a protein called Large ribosomal subunit protein uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	23	139	Total	C	N	O	S	0	0
			1034	648	199	182	5		

- Molecule 54 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	19	180	Total	C	N	O	S	0	0
			1508	933	328	238	9		

- Molecule 55 is a protein called Elongation factor 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	v	847	Total	C	N	O	S	0	0
			6625	4207	1138	1236	44		

- Molecule 56 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	S3	228	Total	C	N	O	S	0	0
			1768	1126	318	316	8		

- Molecule 57 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	FF	149	Total	C	N	O	S	0	0
			1202	770	228	203	1		

- Molecule 58 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	S8	206	Total	C	N	O	S	0	0
			1686	1058	332	291	5		

- Molecule 59 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	S2	221	Total	C	N	O	S	0	0
			1716	1111	295	301	9		

- Molecule 60 is a protein called 40S_SA_C domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	BB	217	Total	C	N	O	S	0	0
			1710	1086	300	316	8		

- Molecule 61 is a protein called eS26.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	UU	101	Total	C	N	O	S	0	0
			814	507	170	132	5		

- Molecule 62 is a protein called eS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	PP	83	Total	C	N	O	S	0	0
			636	393	117	121	5		

- Molecule 63 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	JJ	132	Total	C	N	O	S	0	0
			1068	670	199	195	4		

- Molecule 64 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	AS	213	Total	C	N	O	S	0	0
			1729	1098	309	308	14		

- Molecule 65 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	VV	83	Total	C	N	O	S	0	0
			651	408	121	115	7		

- Molecule 66 is a protein called 40S ribosomal protein S15a.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	QQ	129	Total	C	N	O	S	0	0
			1034	659	193	176	6		

- Molecule 67 is a protein called Large ribosomal subunit protein eL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	24	100	Total	C	N	O	S	0	0
			816	512	164	136	4		

- Molecule 68 is a protein called Large ribosomal subunit protein eL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	30	114	Total	C	N	O	S	0	0
			884	557	156	164	7		

- Molecule 69 is a protein called 40S ribosomal protein S27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	ZZ	68	Total	C	N	O	S	0	0
			555	351	103	94	7		

- Molecule 70 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	18	1662	Total	C	N	O	P	0	0
			35486	15841	6374	11610	1661		

- Molecule 71 is a protein called Small ribosomal subunit protein eS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	MM	141	Total	C	N	O	S	0	0
			1097	688	211	195	3		

- Molecule 72 is a protein called Receptor of activated protein C kinase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	AA	313	Total	C	N	O	S	0	0
			2436	1535	424	465	12		

- Molecule 73 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	OO	100	Total	C	N	O	S	0	0
			795	498	152	141	4		

- Molecule 74 is a protein called SERBP1.

Mol	Chain	Residues	Atoms				AltConf	Trace
74	RB	58	Total	C	N	O	0	0
			459	273	93	93		

- Molecule 75 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	EE	117	Total	C	N	O	S	0	0
			908	570	161	169	8		

- Molecule 76 is a protein called 40S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	CC	96	Total	C	N	O	S	0	0
			810	530	143	131	6		

- Molecule 77 is a protein called Small ribosomal subunit protein uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	II	142	Total	C	N	O	S	0	0
			1128	717	213	195	3		

- Molecule 78 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	TT	75	Total	C	N	O	S	0	0
			598	382	111	104	1		

- Molecule 79 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	WW	62	Total	C	N	O	S	0	0
			488	297	97	92	2		

- Molecule 80 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	XX	55	Total	C	N	O	S	0	0
			459	286	94	74	5		

- Molecule 81 is a protein called Eukaryotic translation initiation factor 5A-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	B	149	Total	C	N	O	S	0	0
			1144	715	195	226	8		

- Molecule 82 is a protein called Ribosomal protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	u	217	Total	C	N	O	S	0	0
			1743	1114	314	306	9		

- Molecule 83 is a protein called Small ribosomal subunit protein uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	S5	185	Total	C	N	O	S	0	0
			1471	921	277	266	7		

- Molecule 84 is a protein called Small ribosomal subunit protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	A	131	Total	C	N	O	S	0	0
			1079	685	205	182	7		

- Molecule 85 is a protein called uL11.

Mol	Chain	Residues	Atoms					AltConf	Trace
85	t	153	Total	C	N	O	S	0	0
			1160	722	218	217	3		

- Molecule 86 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
86	28	3498	Total	C	N	O	P	0	0
			75019	33410	13742	24369	3498		

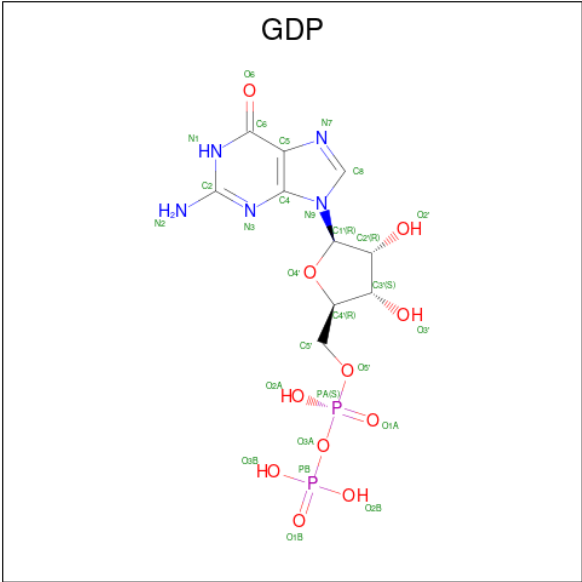
- Molecule 87 is a RNA chain called ES27L.

Mol	Chain	Residues	Atoms					AltConf	Trace
87	ES	35	Total	C	N	O	P	0	0
			756	335	142	244	35		

- Molecule 88 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
88	34	1	Total	Zn	0
			1	1	
88	37	1	Total	Zn	0
			1	1	
88	ff	1	Total	Zn	0
			1	1	
88	GG	1	Total	Zn	0
			1	1	
88	ZZ	1	Total	Zn	0
			1	1	

- Molecule 89 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: C₁₀H₁₅N₅O₁₁P₂) (labeled as "Ligand of Interest" by depositor).

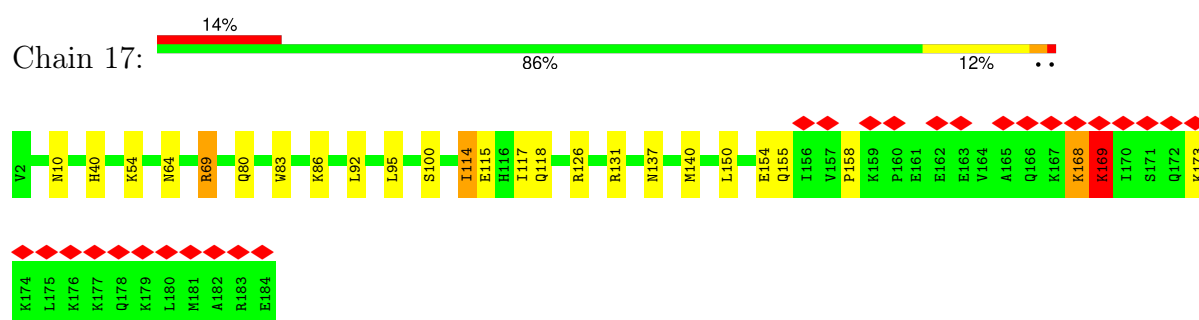


Mol	Chain	Residues	Atoms					AltConf
89	v	1	Total	C	N	O	P	0
			28	10	5	11	2	

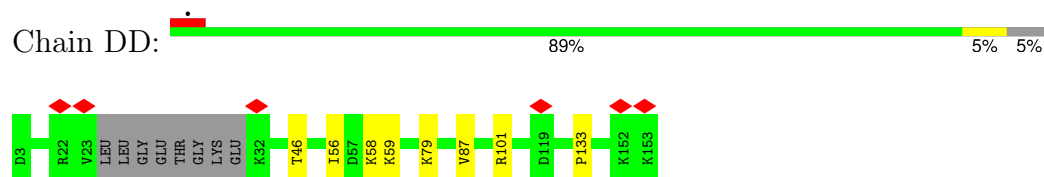
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

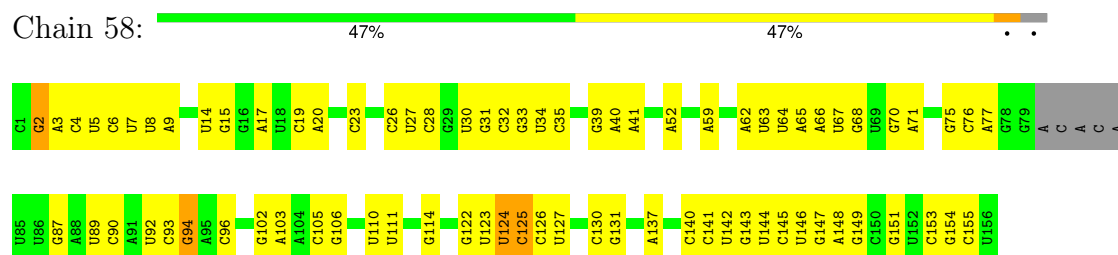
- Molecule 1: Large ribosomal subunit protein uL22



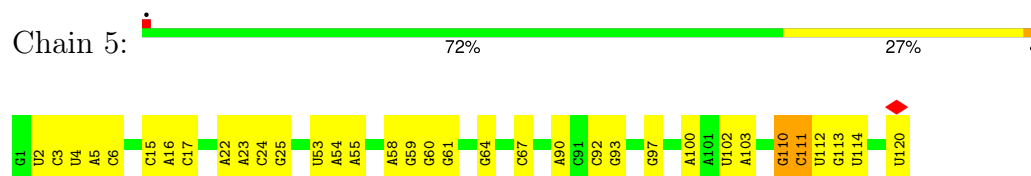
- Molecule 2: Small ribosomal subunit protein uS17



- Molecule 3: 5.8S rRNA

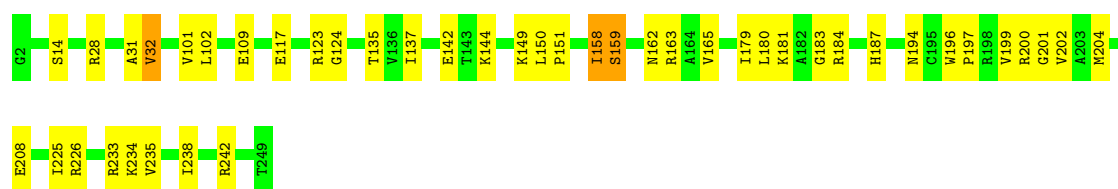


- Molecule 4: 5S rRNA



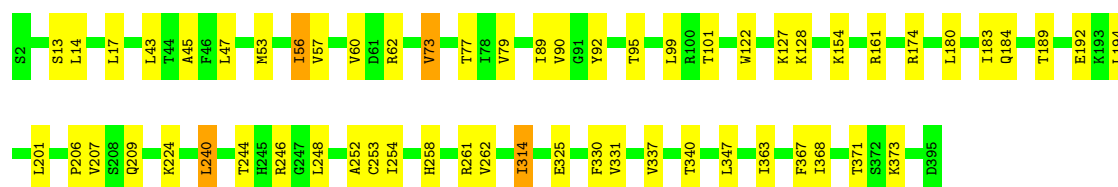
- Molecule 5: 60S ribosomal protein L8

Chain L8:  82% 17%



- Molecule 6: 60S ribosomal protein L3

Chain L3:  85% 14%



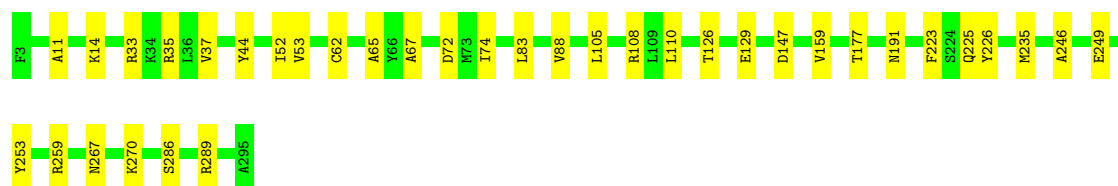
- Molecule 7: 60S ribosomal protein L4

Chain L4:  87% 12%



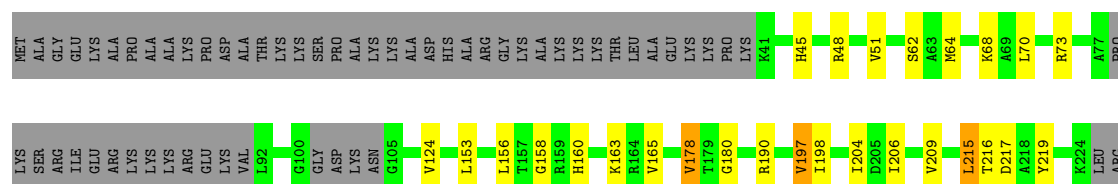
- Molecule 8: 60S ribosomal protein L5

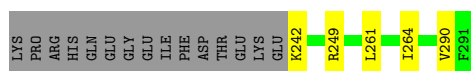
Chain L5:  88% 12%



- Molecule 9: 60S ribosomal protein L6

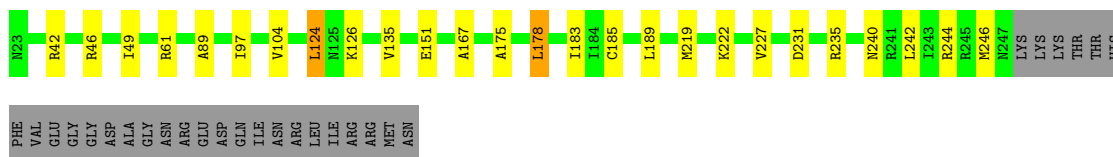
Chain L6:  63% 10% 26%





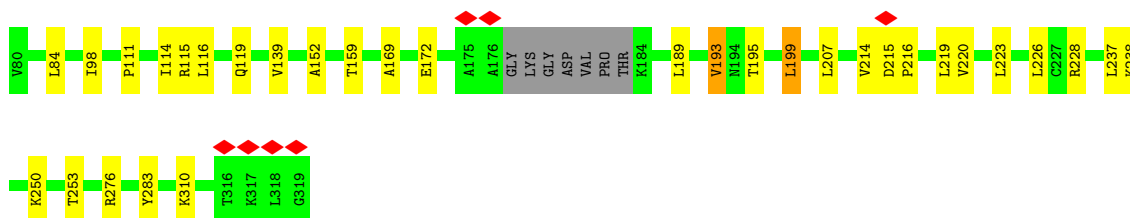
- Molecule 10: 60S ribosomal protein L7

Chain L7: 79% 9% 11%



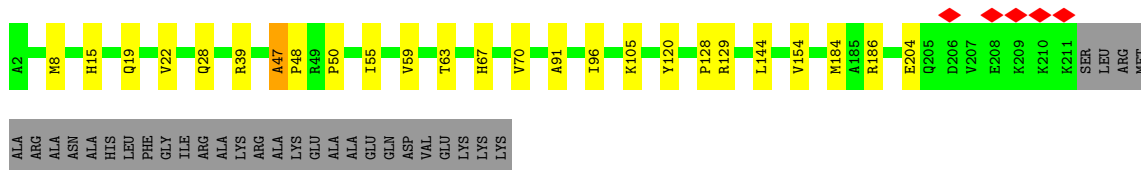
- Molecule 11: Large ribosomal subunit protein eL8

Chain aa: 84% 12%



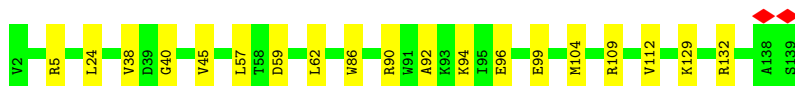
- Molecule 12: Large ribosomal subunit protein eL13

Chain 13: 77% 10% 13%



- Molecule 13: 60S ribosomal protein L14

Chain 14: 86% 14%



- Molecule 14: 60S ribosomal protein L15

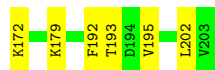
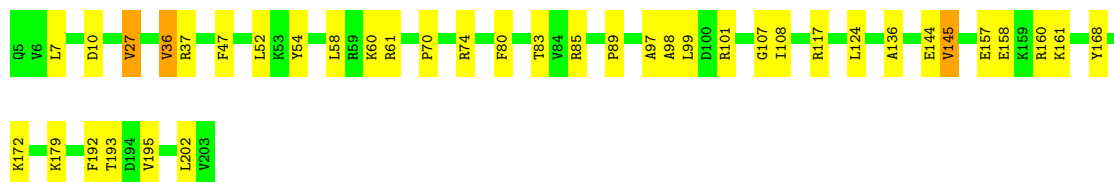
Chain 15: 80% 19%





- Molecule 15: Large ribosomal subunit protein uL13

Chain bb: 80% 18%



- Molecule 16: Large ribosomal subunit protein eL20

Chain 20: 85% 14%



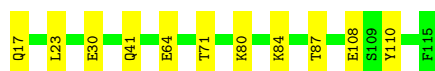
- Molecule 17: 60S ribosomal protein L21

Chain 21: 90% 10%



- Molecule 18: Large ribosomal subunit protein eL22

Chain 22: 89% 11%



- Molecule 19: Large ribosomal subunit protein uL23

Chain cc: 86% 14%



- Molecule 20: 60S ribosomal protein L26

Chain 26: 86% 13%



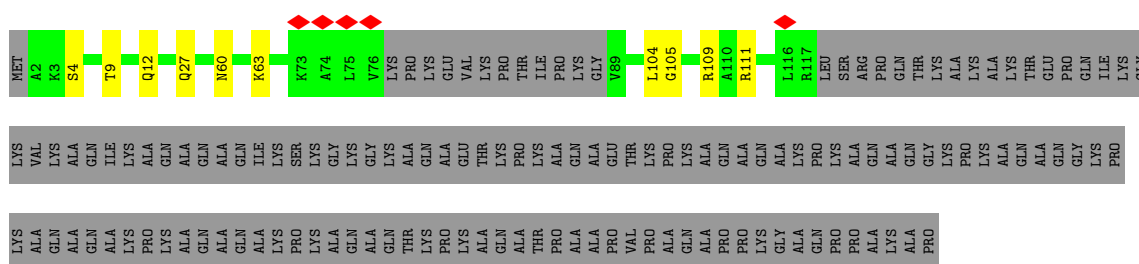
- Molecule 21: 60S ribosomal protein L27



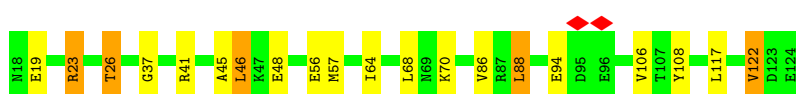
- Molecule 22: 60S ribosomal protein L27a



- Molecule 23: Large ribosomal subunit protein eL29



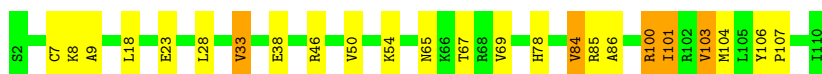
- Molecule 24: 60S ribosomal protein L31



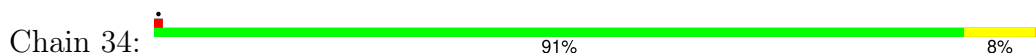
- Molecule 25: Large ribosomal subunit protein eL32

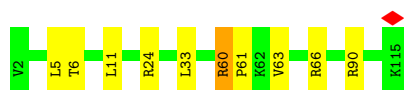


- Molecule 26: Large ribosomal subunit protein eL33

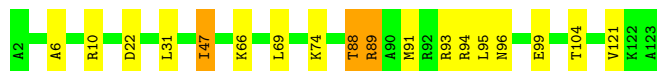
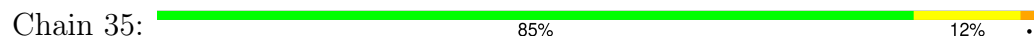


- Molecule 27: 60S ribosomal protein L34





- Molecule 28: 60S ribosomal protein L35



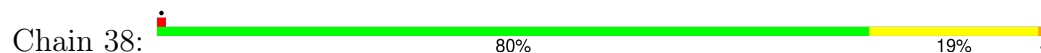
- Molecule 29: 60S ribosomal protein L36



- Molecule 30: 60S ribosomal protein L37



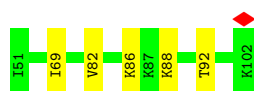
- Molecule 31: Large ribosomal subunit protein eL38



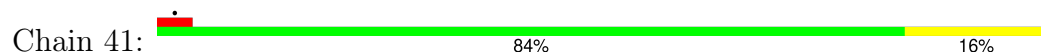
- Molecule 32: 60S ribosomal protein L39

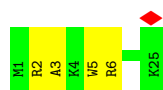


- Molecule 33: Large ribosomal subunit protein eL40



- Molecule 34: eL41





- Molecule 35: eL42

Chain 42: 88% 11%



- Molecule 36: 60S ribosomal protein L37a

Chain ff: 90% 8%



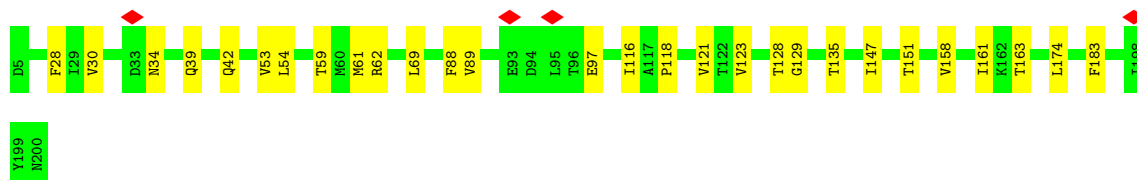
- Molecule 37: 60S ribosomal protein L28

Chain gg: 90% 10%



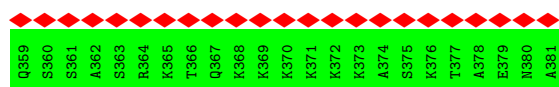
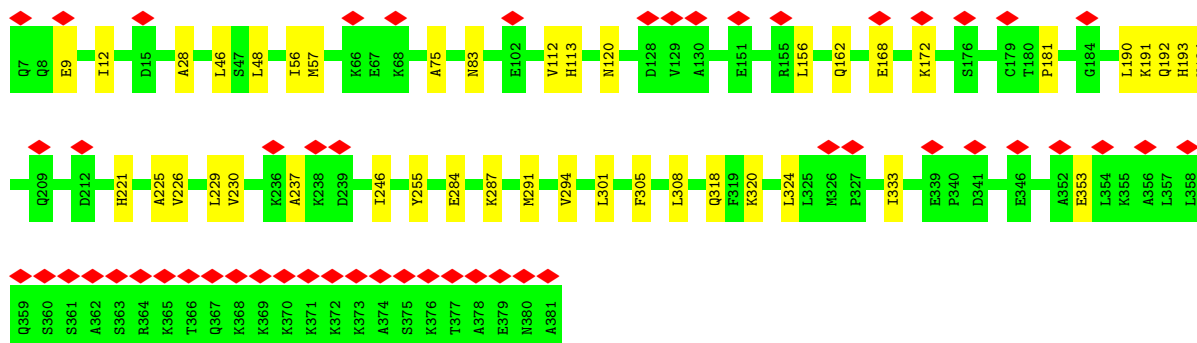
- Molecule 38: 60S acidic ribosomal protein P0

Chain s: 86% 14%



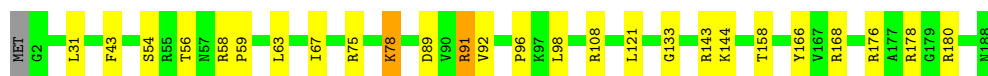
- Molecule 39: Proliferation-associated protein 2G4

Chain EB: 14% 89% 11%



- Molecule 40: Large ribosomal subunit protein eL18

Chain Q:  86% 13% ..



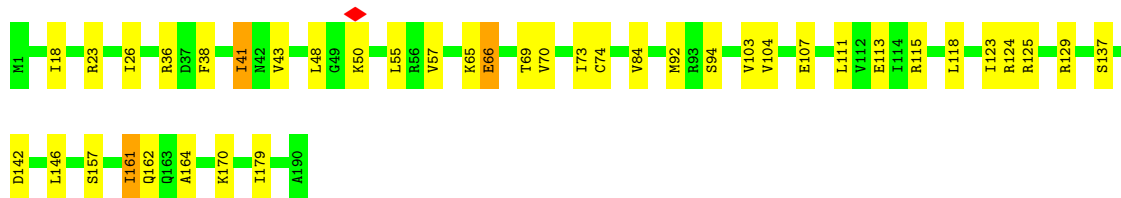
- Molecule 41: Ribosomal protein L10

Chain 10:  80% 17% ..



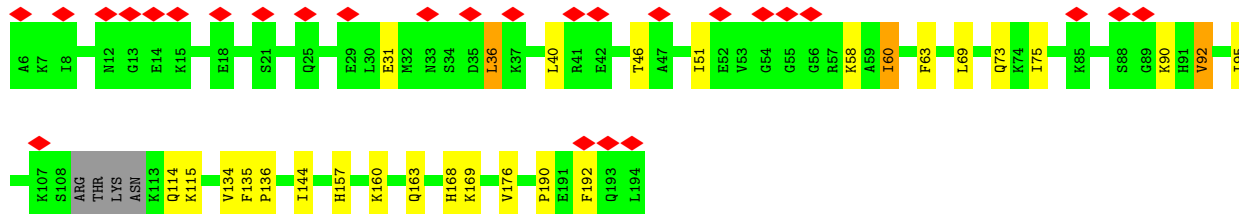
- Molecule 42: 60S ribosomal protein L9

Chain L9:  79% 19% .



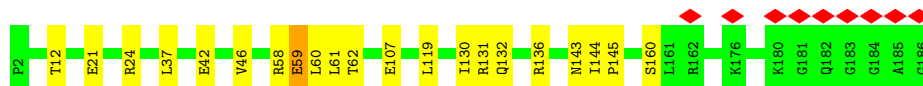
- Molecule 43: Small ribosomal subunit protein eS7

Chain S7:  14% 83% 13% ..

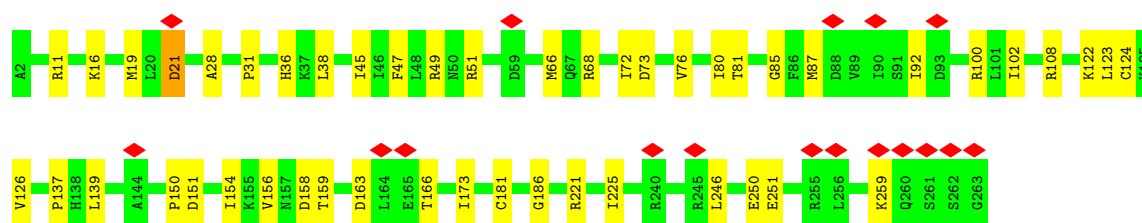
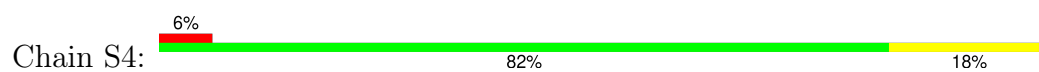


- Molecule 44: 40S ribosomal protein S9

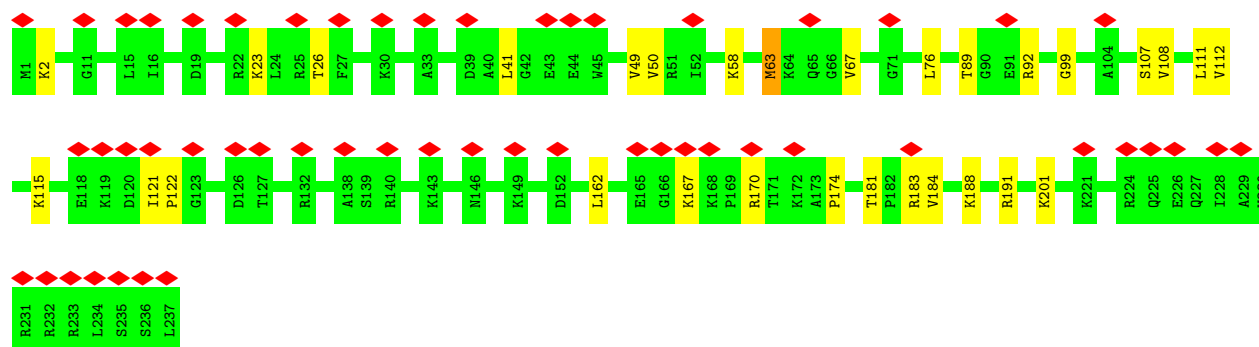
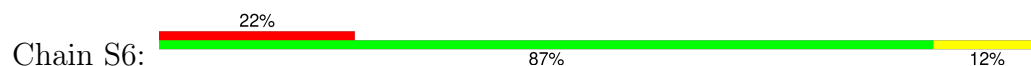
Chain S9:  5% 89% 11% .



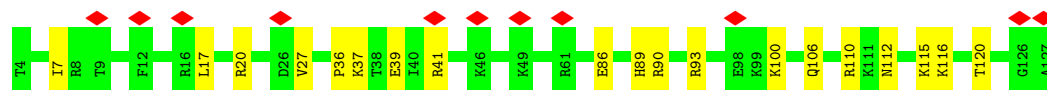
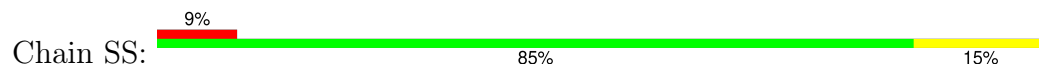
- Molecule 45: 40S ribosomal protein S4



- Molecule 46: 40S ribosomal protein S6



- Molecule 47: 40S ribosomal protein S24



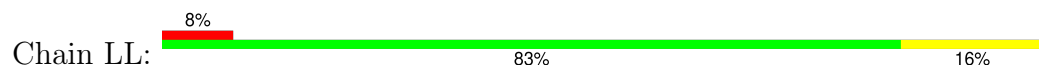
- Molecule 48: 40S ribosomal protein S23

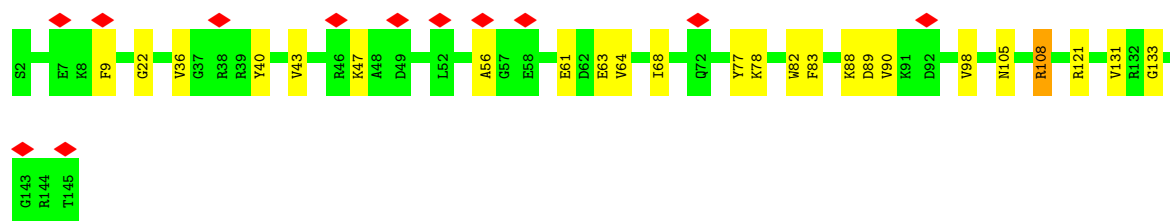


- Molecule 49: 40S ribosomal protein S30



- Molecule 50: 40S ribosomal protein S18





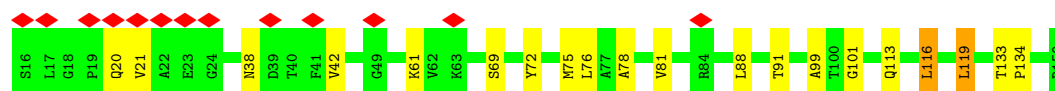
- Molecule 51: 60S ribosomal protein L11

Chain 11: 90% 9% .



- Molecule 52: Small ribosomal subunit protein uS11

Chain GG: 10% 85% 13% .



- Molecule 53: Large ribosomal subunit protein uL14

Chain 23: 92% 8% .



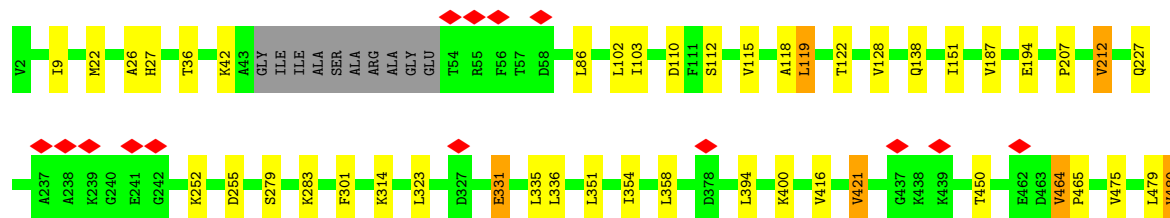
- Molecule 54: 60S ribosomal protein L19

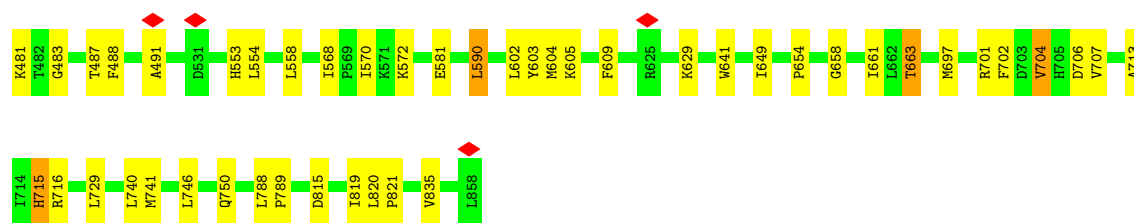
Chain 19: 89% 9% .



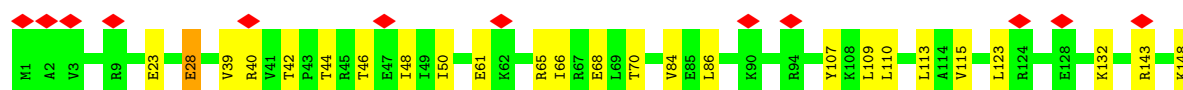
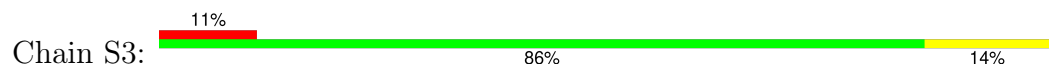
- Molecule 55: Elongation factor 2

Chain v: 88% 10% ..

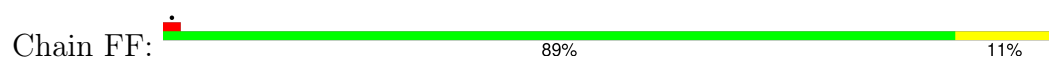




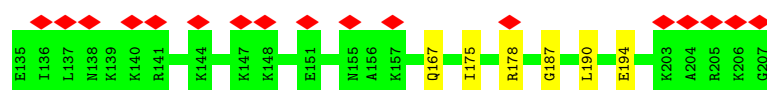
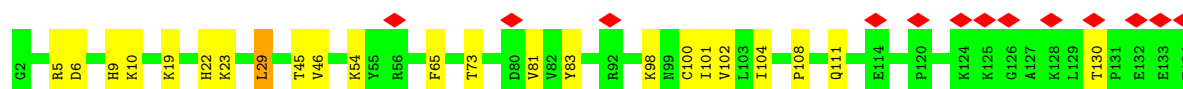
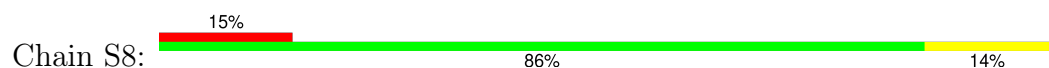
- Molecule 56: 40S ribosomal protein S3



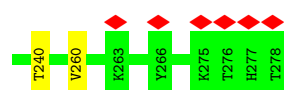
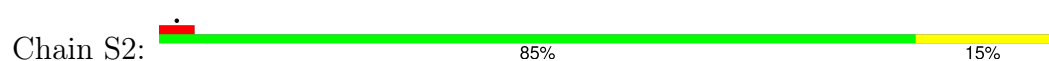
- Molecule 57: 40S ribosomal protein S13



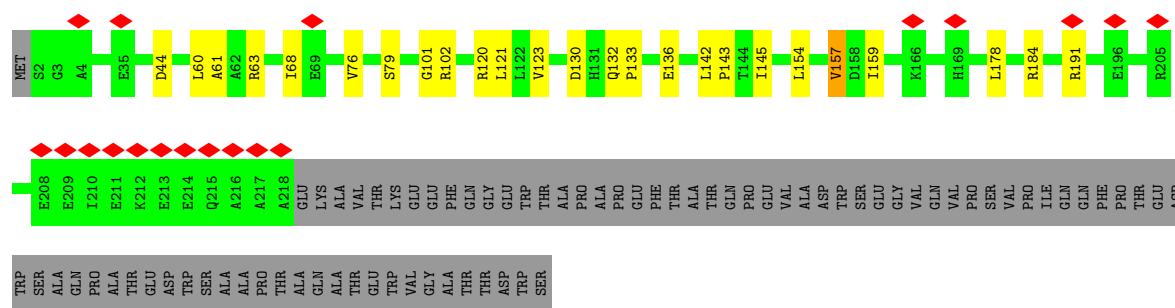
- Molecule 58: 40S ribosomal protein S8



- Molecule 59: 40S ribosomal protein S2



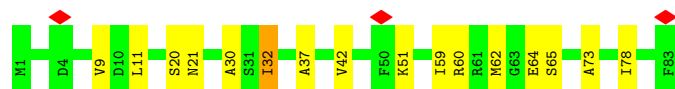
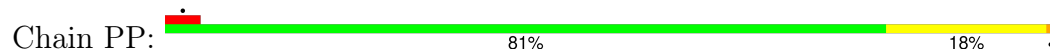
- Molecule 60: 40S_SA_C domain-containing protein



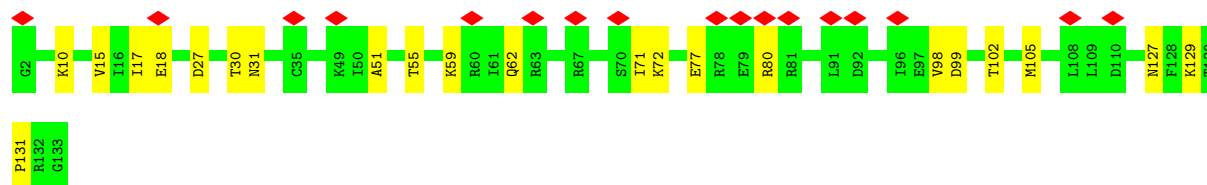
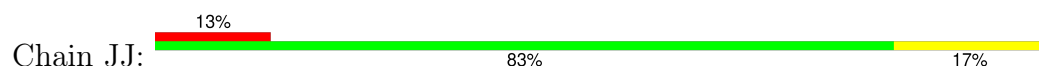
- Molecule 61: eS26



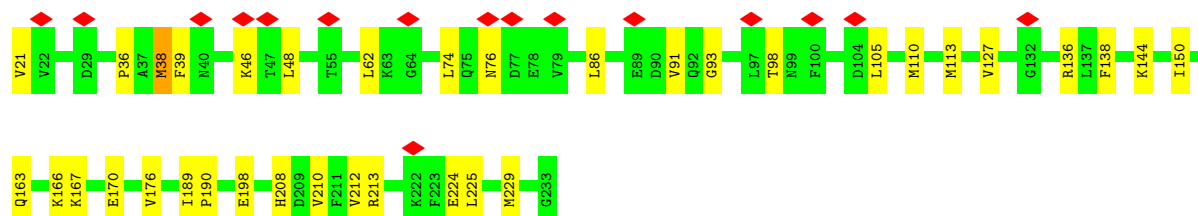
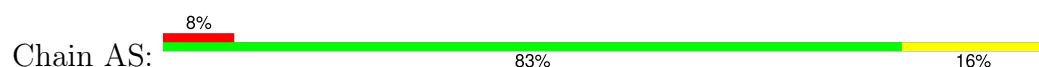
- Molecule 62: eS21



- Molecule 63: 40S ribosomal protein S17



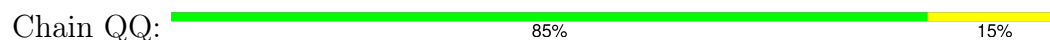
- Molecule 64: 40S ribosomal protein S3a



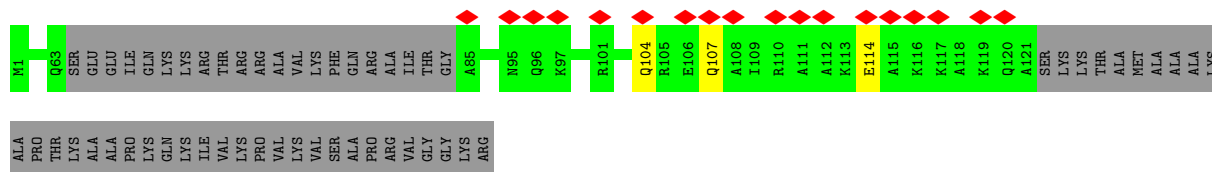
- Molecule 65: 40S ribosomal protein S27



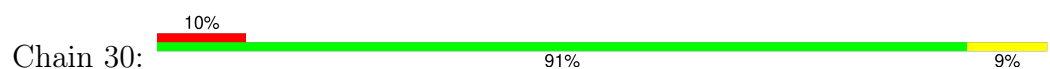
- Molecule 66: 40S ribosomal protein S15a



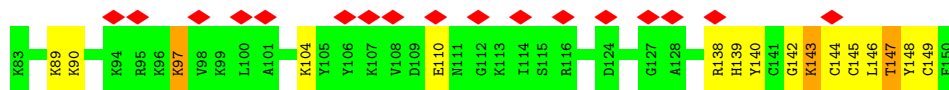
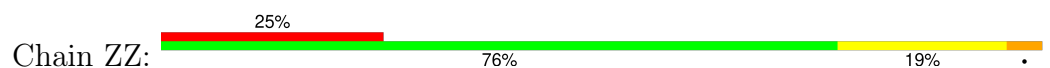
- Molecule 67: Large ribosomal subunit protein eL24



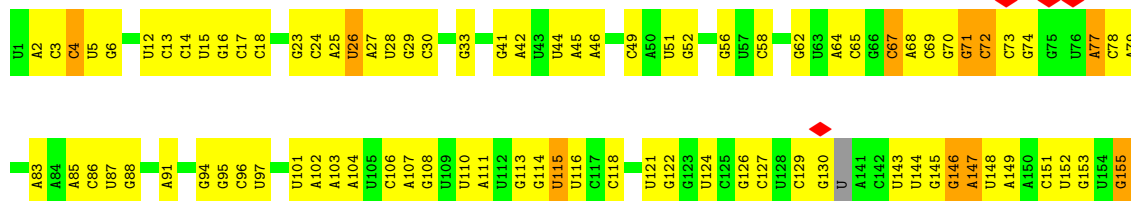
- Molecule 68: Large ribosomal subunit protein eL30

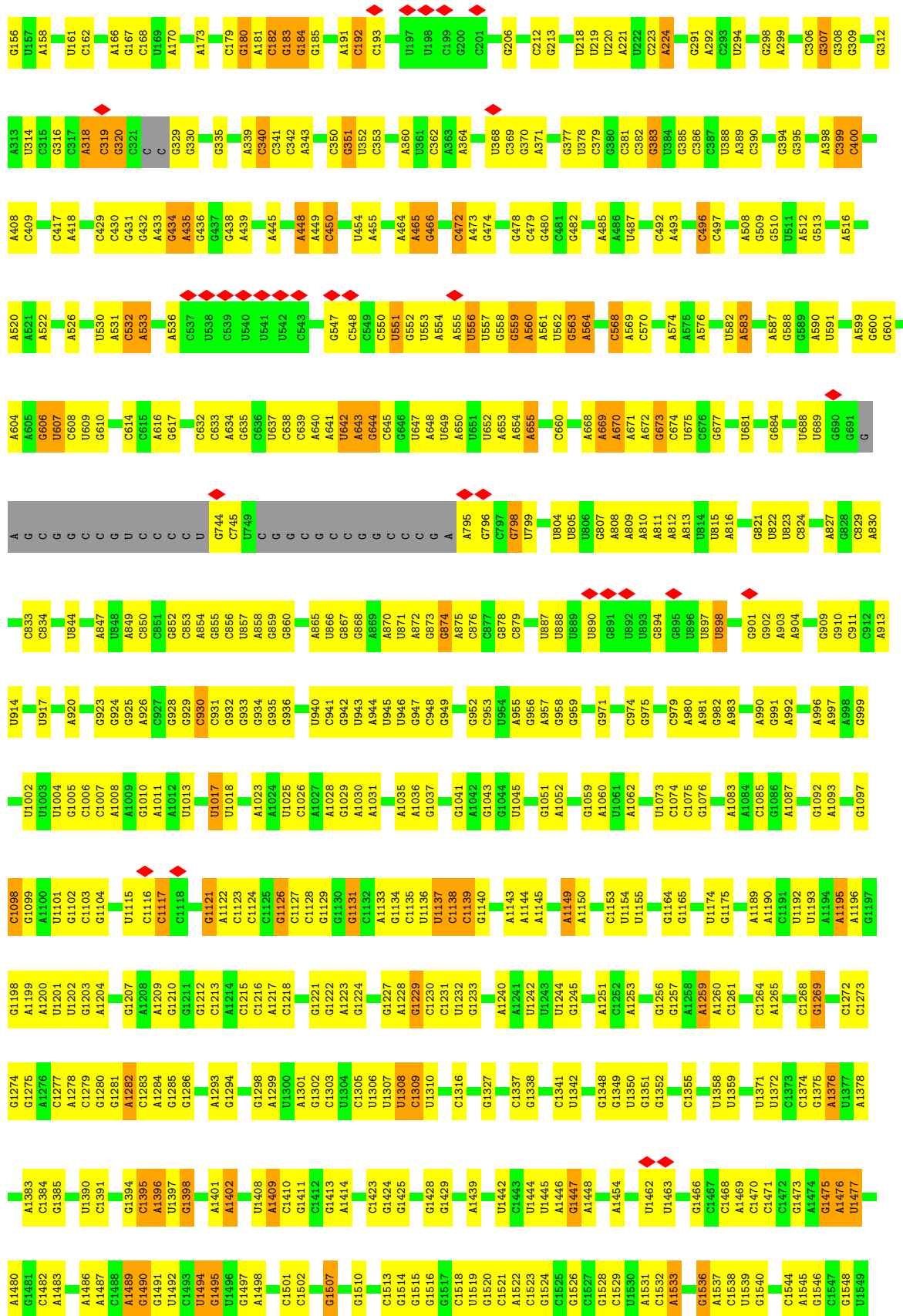


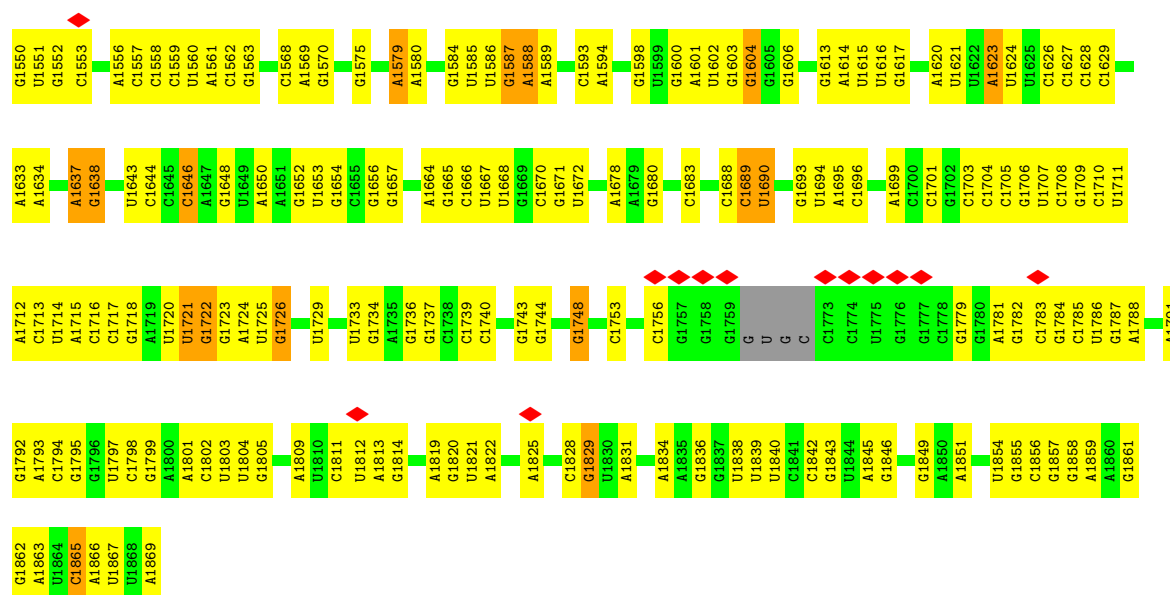
- Molecule 69: 40S ribosomal protein S27a



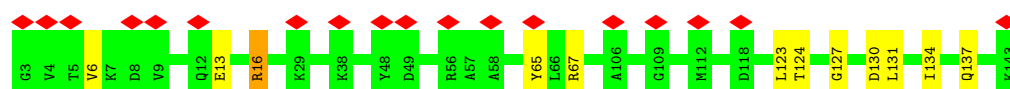
- Molecule 70: 18S rRNA



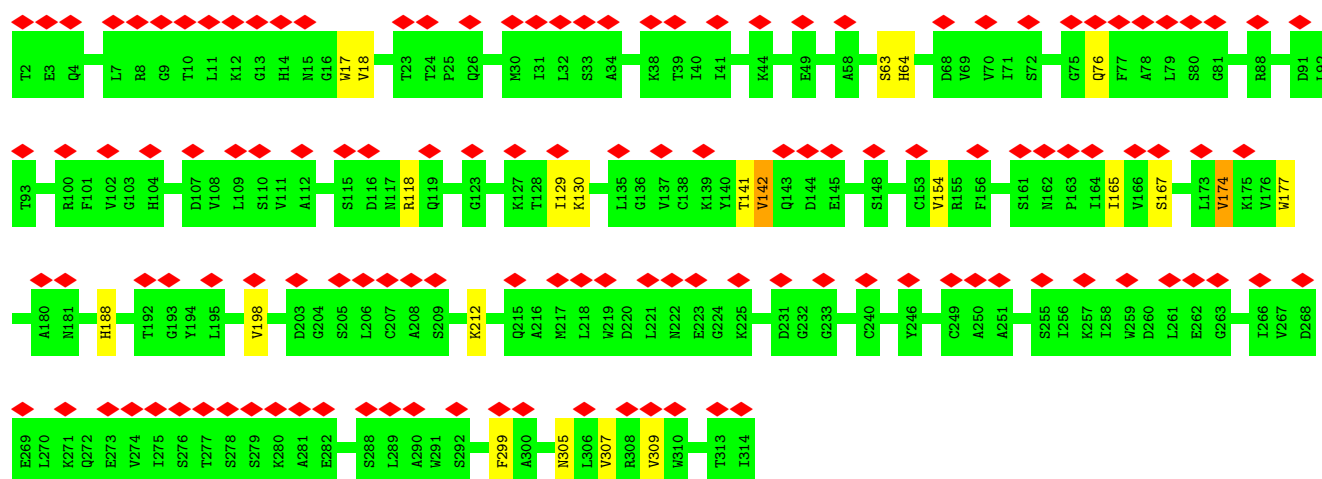




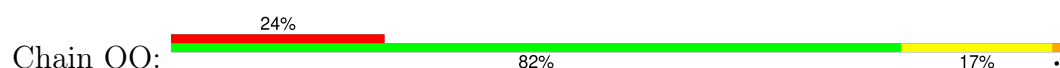
- Molecule 71: Small ribosomal subunit protein eS19

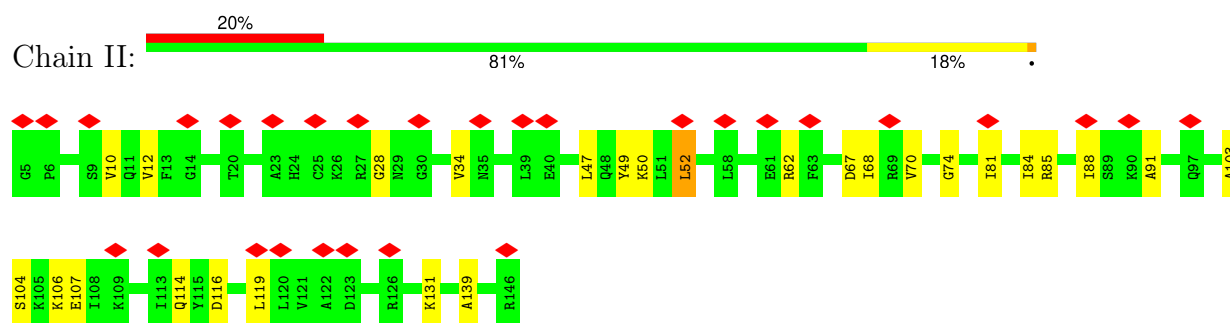


- Molecule 72: Receptor of activated protein C kinase 1

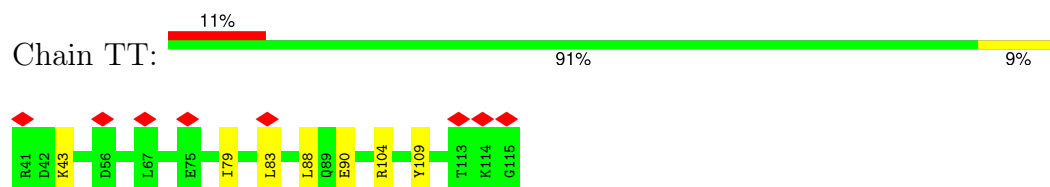


- Molecule 73: 40S ribosomal protein S20

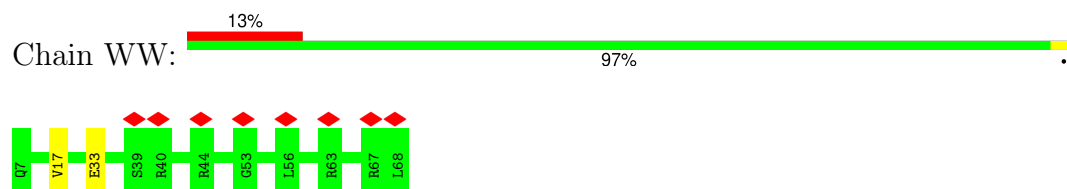




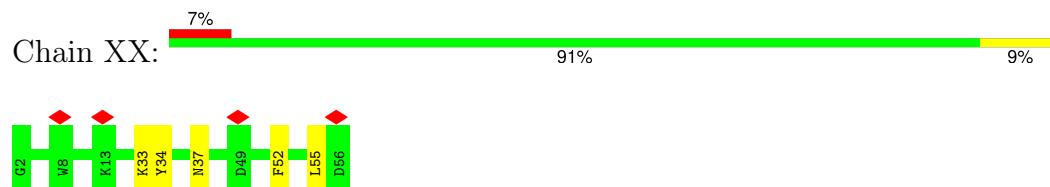
- Molecule 78: 40S ribosomal protein S25



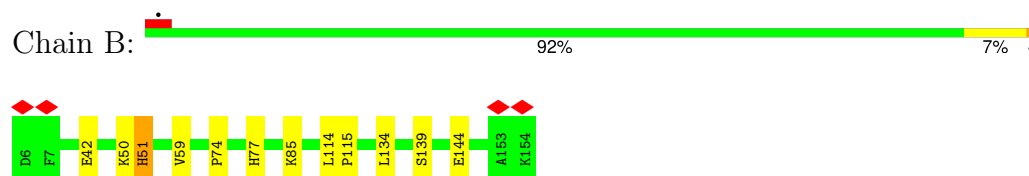
- Molecule 79: 40S ribosomal protein S28



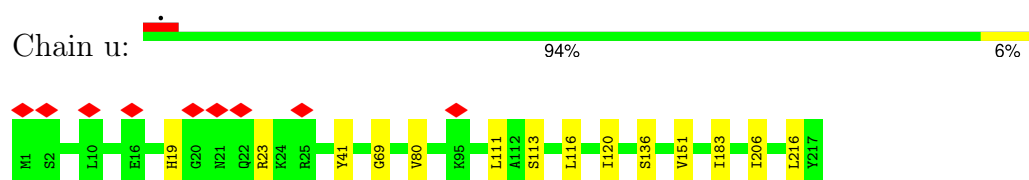
- Molecule 80: 40S ribosomal protein S29



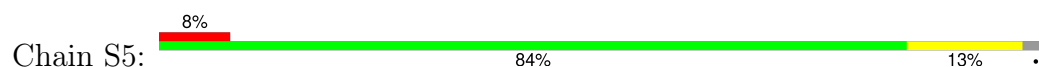
- Molecule 81: Eukaryotic translation initiation factor 5A-1

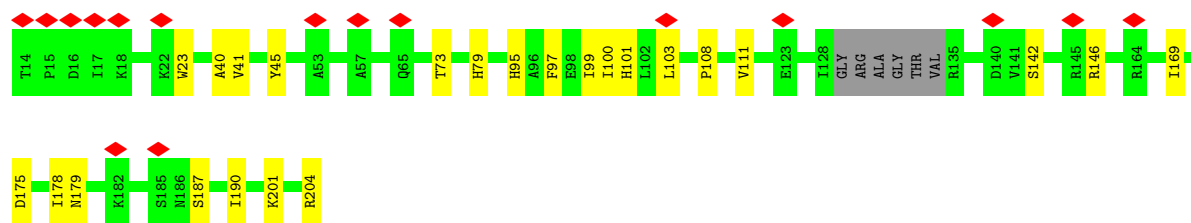


- Molecule 82: Ribosomal protein

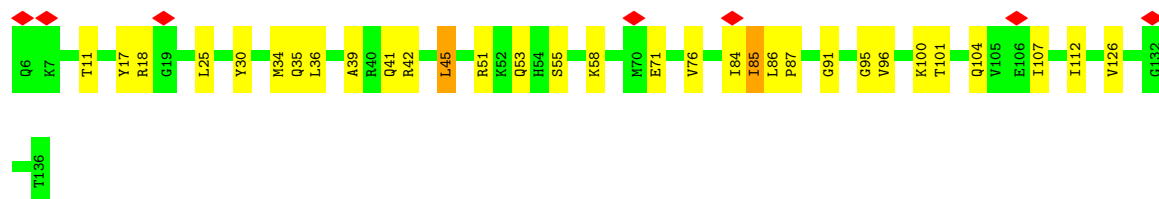
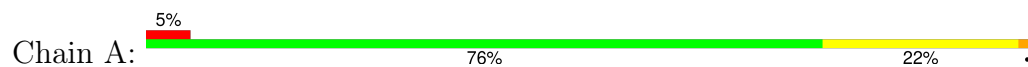


- Molecule 83: Small ribosomal subunit protein uS7

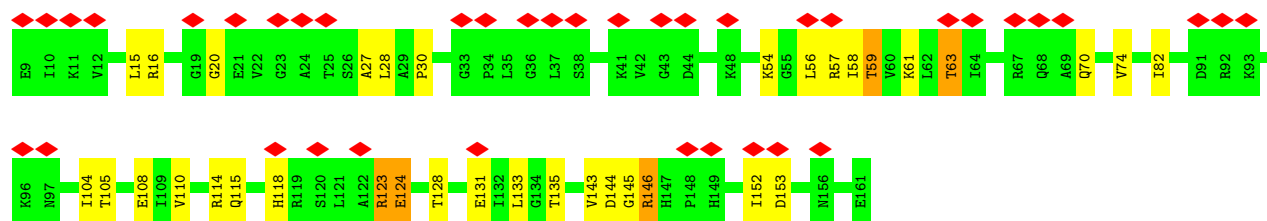
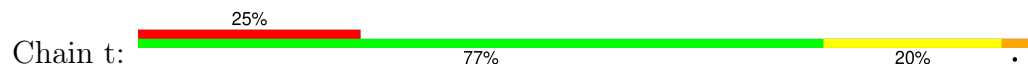




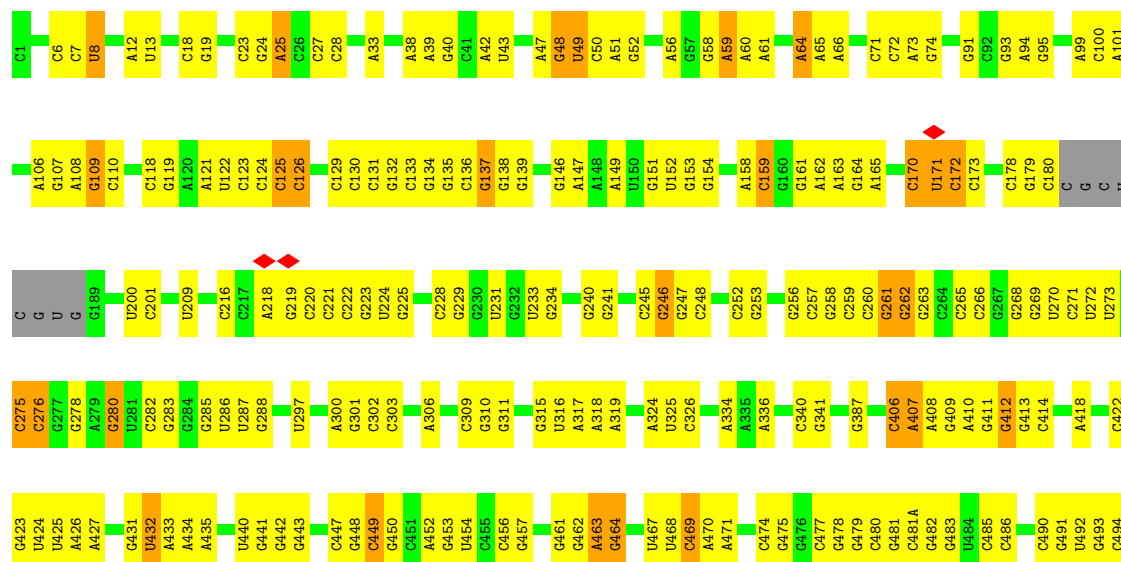
- Molecule 84: Small ribosomal subunit protein uS19



- Molecule 85: uL11



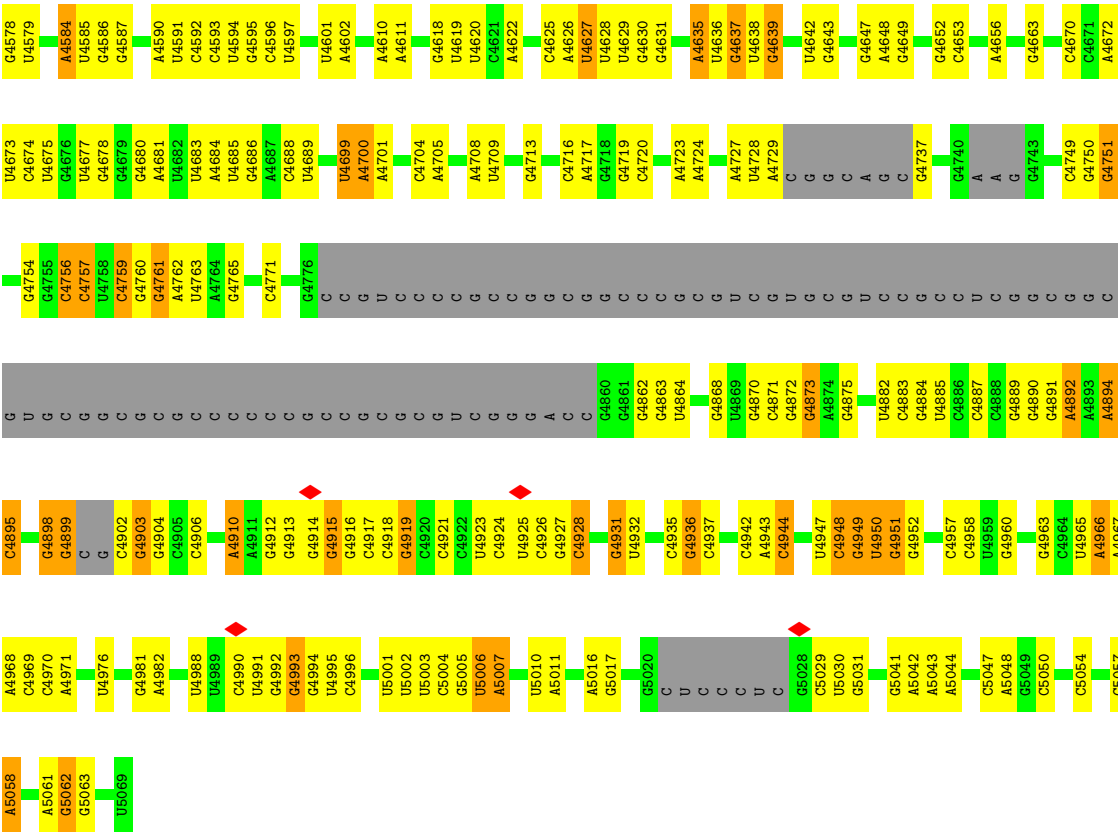
- Molecule 86: 28S rRNA



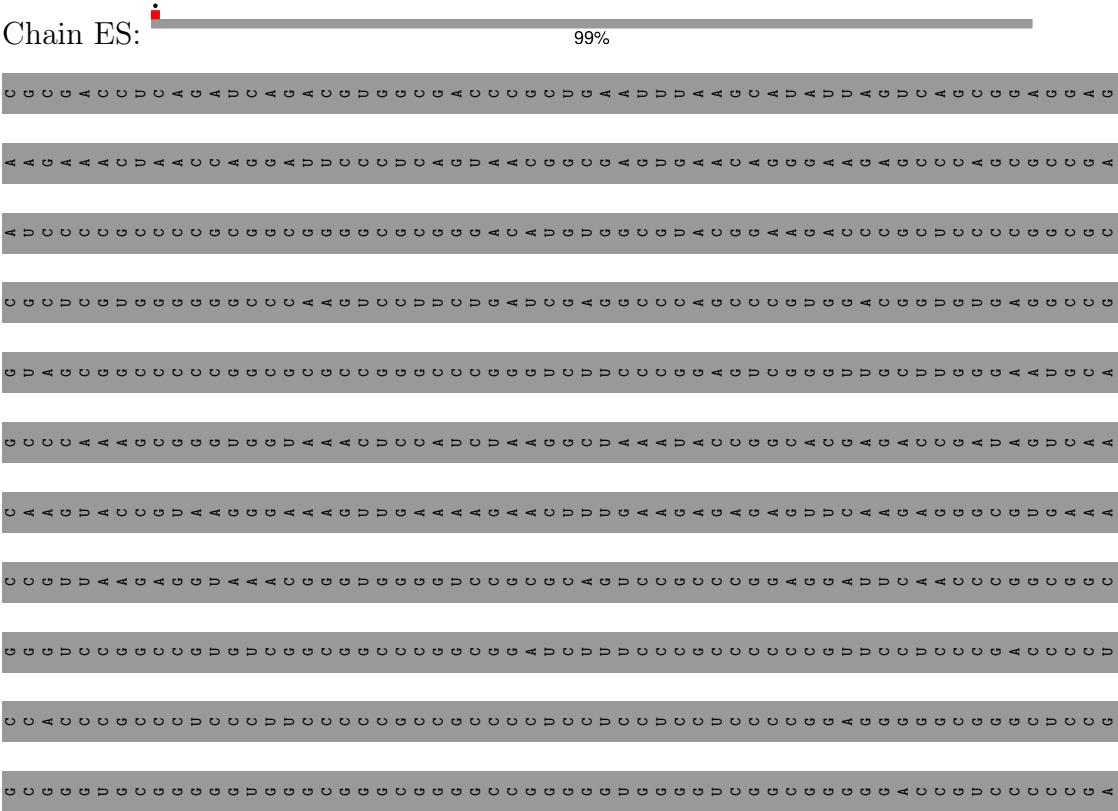


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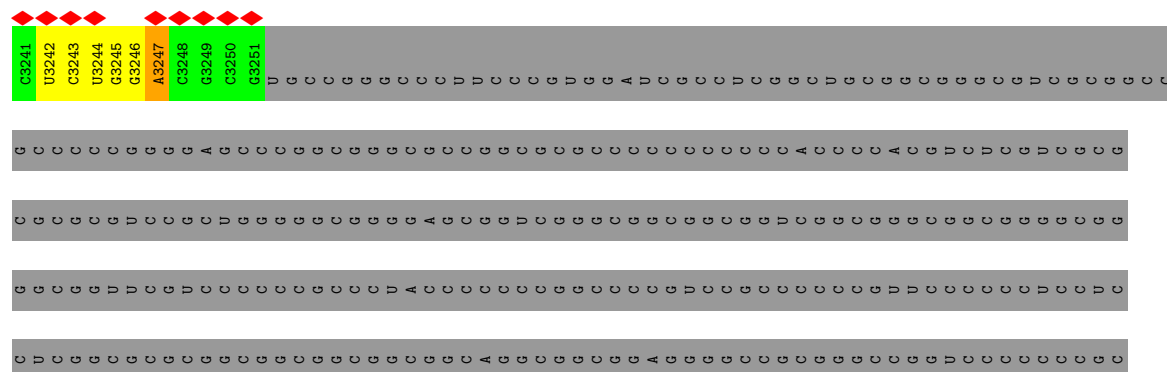




● Molecule 87: ES27L







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C C C G U G G A G C C A A A G G G C C A A A A G C C U C G C C U U G A U C C U U U C G A U U U C C A G U A A C C G

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G G G A G C C U C G G G G G C C C G G G A U A C C G G G C C C C C G G U C C C C G G G G G C C C C

C C C C C C U C C A C G G C C C C G G G G G G A G G C C G C C C C C C C C C G G G A C C C G

G G G U C C G G U G G C G A G U G C C C U U C C G G G G A A C G G G C C G C C G G A A G G C C C G C

C C C C U C C C C G G C A C G G A C C G C C U U C C G G G A A C C U G G C C U A A A C C A U G A A C

G A C C C U G C U U C C G G U C C G G G U U U C C G U A C C G U U A G C C C C C C C C C C C C C U

G A A A G U C A G C C C U C G A A C A A A G G G U U G U G U C

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	157683	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	39	Depositor
Minimum defocus (nm)	700	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	OTHER	Depositor
Maximum map value	36.663	Depositor
Minimum map value	-14.311	Depositor
Average map value	0.004	Depositor
Map value standard deviation	0.783	Depositor
Recommended contour level	2.4	Depositor
Map size ($\text{\AA}$)	664.0, 664.0, 664.0	wwPDB
Map dimensions	800, 800, 800	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.83, 0.83, 0.83	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: DDE, GDP, ZN, 5CT

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	17	0.15	0/1518	0.48	2/2029 (0.1%)
2	DD	0.11	0/1195	0.29	0/1597
3	58	0.13	0/3581	0.30	0/5577
4	5	0.12	0/2858	0.27	0/4455
5	L8	0.13	0/1936	0.36	0/2596
6	L3	0.13	0/3240	0.34	0/4339
7	L4	0.12	0/2937	0.33	0/3946
8	L5	0.12	0/2437	0.32	0/3264
9	L6	0.12	0/1762	0.33	0/2362
10	L7	0.12	0/1910	0.31	0/2549
11	aa	0.13	0/1910	0.36	0/2569
12	13	0.13	0/1732	0.35	0/2316
13	14	0.13	0/1158	0.34	0/1547
14	15	0.13	0/1746	0.36	0/2338
15	bb	0.15	0/1662	0.35	0/2222
16	20	0.14	0/1501	0.36	0/2012
17	21	0.12	0/1326	0.31	0/1770
18	22	0.14	0/823	0.37	0/1104
19	cc	0.11	0/984	0.31	0/1323
20	26	0.11	0/1132	0.32	0/1504
21	27	0.13	0/1130	0.34	0/1507
22	dd	0.13	0/1191	0.34	0/1590
23	29	0.12	0/861	0.32	0/1138
24	31	0.12	0/903	0.34	0/1216
25	32	0.12	0/1071	0.33	0/1429
26	ee	0.14	0/895	0.37	0/1198
27	34	0.11	0/916	0.30	0/1220
28	35	0.12	0/1021	0.34	0/1348
29	36	0.11	0/841	0.30	0/1112
30	37	0.13	0/720	0.37	0/952
31	38	0.13	0/575	0.36	0/761
32	39	0.12	0/459	0.32	0/608

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	40	0.11	0/435	0.31	0/575
34	41	0.14	0/240	0.34	0/305
35	42	0.12	0/864	0.35	0/1140
36	ff	0.13	0/718	0.38	0/953
37	gg	0.13	0/1006	0.33	0/1349
38	s	0.14	0/1530	0.35	0/2064
39	EB	0.14	0/2979	0.36	1/4000 (0.0%)
40	Q	0.13	0/1538	0.38	0/2054
41	10	0.13	0/1734	0.35	0/2315
42	L9	0.14	0/1535	0.38	0/2063
43	S7	0.14	0/1510	0.35	0/2022
44	S9	0.13	0/1550	0.34	0/2069
45	S4	0.12	0/2118	0.34	0/2849
46	S6	0.13	0/1946	0.31	0/2590
47	SS	0.13	0/1028	0.32	0/1366
48	RR	0.13	0/1116	0.42	2/1490 (0.1%)
49	YY	0.13	0/447	0.34	0/587
50	LL	0.15	0/1208	0.40	0/1618
51	11	0.13	0/1385	0.39	0/1852
52	GG	0.12	0/1020	0.35	0/1369
53	23	0.11	0/1048	0.33	0/1402
54	19	0.12	0/1524	0.31	0/2013
55	v	0.13	0/6733	0.34	0/9091
56	S3	0.14	0/1796	0.35	0/2417
57	FF	0.12	0/1226	0.30	0/1649
58	S8	0.13	0/1715	0.36	0/2287
59	S2	0.14	0/1753	0.35	0/2369
60	BB	0.12	0/1747	0.33	0/2374
61	UU	0.12	0/828	0.34	0/1109
62	PP	0.12	0/643	0.31	0/860
63	JJ	0.15	0/1082	0.37	0/1452
64	AS	0.12	0/1756	0.32	0/2350
65	VV	0.11	0/665	0.31	0/891
66	QQ	0.14	0/1051	0.36	0/1406
67	24	0.12	0/829	0.31	0/1099
68	30	0.13	0/895	0.33	0/1196
69	ZZ	0.13	0/567	0.39	0/753
70	18	0.11	0/39682	0.31	0/61841
71	MM	0.14	0/1115	0.33	0/1493
72	AA	0.13	0/2493	0.34	0/3394
73	OO	0.12	0/805	0.33	0/1081
74	RB	0.11	0/466	0.27	0/616
75	EE	0.14	0/918	0.38	0/1233

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	CC	0.16	0/834	0.43	0/1125
77	II	0.14	0/1146	0.35	0/1534
78	TT	0.14	0/604	0.30	0/810
79	WW	0.15	0/490	0.40	0/656
80	XX	0.10	0/470	0.31	0/623
81	B	0.15	0/1144	0.36	0/1535
82	u	0.11	0/1771	0.30	0/2375
83	S5	0.13	0/1492	0.32	0/2005
84	A	0.15	0/1099	0.38	0/1465
85	t	0.16	0/1174	0.45	0/1582
86	28	0.14	0/83916	0.33	0/130870
87	ES	0.15	0/844	0.40	0/1314
All	All	0.13	0/240159	0.33	5/350398 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	17	0	1

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	17	168	LYS	CA-C-N	7.83	135.80	121.70
1	17	168	LYS	C-N-CA	7.83	135.80	121.70
48	RR	60	LYS	CA-C-N	5.63	130.05	121.03
48	RR	60	LYS	C-N-CA	5.63	130.05	121.03
39	EB	83	ASN	CB-CA-C	-5.07	110.34	117.23

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	17	169	LYS	Peptide

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	17	1490	0	1560	17	0
2	DD	1175	0	1249	3	0
3	58	3208	0	1629	49	0
4	5	2558	0	1296	24	0
5	L8	1898	0	1993	28	0
6	L3	3172	0	3310	28	0
7	L4	2883	0	3053	27	0
8	L5	2391	0	2424	19	0
9	L6	1729	0	1887	21	0
10	L7	1874	0	1995	18	0
11	aa	1879	0	2027	15	0
12	13	1701	0	1820	14	0
13	14	1137	0	1211	8	0
14	15	1701	0	1749	26	0
15	bb	1630	0	1778	23	0
16	20	1462	0	1508	10	0
17	21	1298	0	1366	9	0
18	22	809	0	833	3	0
19	cc	967	0	1040	7	0
20	26	1115	0	1205	7	0
21	27	1107	0	1182	8	0
22	dd	1162	0	1209	11	0
23	29	848	0	920	5	0
24	31	888	0	930	11	0
25	32	1053	0	1147	7	0
26	ee	876	0	912	16	0
27	34	906	0	998	7	0
28	35	1013	0	1147	11	0
29	36	830	0	916	3	0
30	37	705	0	737	5	0
31	38	569	0	637	7	0
32	39	447	0	480	3	0
33	40	429	0	469	3	0
34	41	239	0	289	2	0
35	42	851	0	924	6	0
36	ff	708	0	756	4	0
37	gg	990	0	1044	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	s	1507	0	1564	12	0
39	EB	2932	0	2967	16	0
40	Q	1514	0	1634	15	0
41	10	1696	0	1745	19	0
42	L9	1516	0	1597	17	0
43	S7	1488	0	1582	16	0
44	S9	1525	0	1640	12	0
45	S4	2076	0	2177	27	0
46	S6	1923	0	2089	19	0
47	SS	1011	0	1083	10	0
48	RR	1098	0	1167	11	0
49	YY	443	0	492	4	0
50	LL	1190	0	1249	14	0
51	11	1362	0	1399	7	0
52	GG	1007	0	1028	10	0
53	23	1034	0	1097	7	0
54	19	1508	0	1664	9	0
55	v	6625	0	6705	43	0
56	S3	1768	0	1866	18	0
57	FF	1202	0	1289	6	0
58	S8	1686	0	1772	17	0
59	S2	1716	0	1806	15	0
60	BB	1710	0	1708	13	0
61	UU	814	0	864	5	0
62	PP	636	0	637	10	0
63	JJ	1068	0	1121	12	0
64	AS	1729	0	1803	20	0
65	VV	651	0	672	4	0
66	QQ	1034	0	1080	14	0
67	24	816	0	856	1	0
68	30	884	0	931	3	0
69	ZZ	555	0	567	12	0
70	18	35486	0	17916	525	0
71	MM	1097	0	1132	6	0
72	AA	2436	0	2393	8	0
73	OO	795	0	862	9	0
74	RB	459	0	421	8	0
75	EE	908	0	939	6	0
76	CC	810	0	836	9	0
77	II	1128	0	1195	14	0
78	TT	598	0	656	6	0
79	WW	488	0	514	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
80	XX	459	0	452	3	0
81	B	1144	0	1148	6	0
82	u	1743	0	1859	7	0
83	S5	1471	0	1522	10	0
84	A	1079	0	1141	19	0
85	t	1160	0	1218	18	0
86	28	75019	0	37897	1064	0
87	ES	756	0	384	22	0
88	34	1	0	0	0	0
88	37	1	0	0	0	0
88	GG	1	0	0	0	0
88	ZZ	1	0	0	0	0
88	ff	1	0	0	0	0
89	v	28	0	12	0	0
All	All	224491	0	171978	2417	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 6.

The worst 5 of 2417 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:17:168:LYS:HA	1:17:169:LYS:HB2	1.46	0.95
56:S3:143:ARG:HH21	74:RB:218:TRP:HB2	1.33	0.93
86:28:2465:C:H1'	86:28:3672:G:H22	1.35	0.92
70:18:1723:G:H2'	70:18:1724:A:H8	1.37	0.86
13:14:40:GLY:HA3	13:14:45:VAL:HB	1.56	0.86

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	17	181/183 (99%)	177 (98%)	3 (2%)	1 (1%)	21	32
2	DD	139/151 (92%)	136 (98%)	3 (2%)	0	100	100
5	L8	246/248 (99%)	237 (96%)	8 (3%)	1 (0%)	30	43
6	L3	392/394 (100%)	381 (97%)	11 (3%)	0	100	100
7	L4	360/362 (99%)	351 (98%)	9 (2%)	0	100	100
8	L5	291/293 (99%)	284 (98%)	7 (2%)	0	100	100
9	L6	208/291 (72%)	201 (97%)	7 (3%)	0	100	100
10	L7	223/253 (88%)	218 (98%)	5 (2%)	0	100	100
11	aa	229/240 (95%)	223 (97%)	6 (3%)	0	100	100
12	13	208/241 (86%)	203 (98%)	3 (1%)	2 (1%)	12	20
13	14	136/138 (99%)	134 (98%)	2 (2%)	0	100	100
14	15	201/203 (99%)	196 (98%)	5 (2%)	0	100	100
15	bb	197/199 (99%)	194 (98%)	3 (2%)	0	100	100
16	20	174/176 (99%)	170 (98%)	4 (2%)	0	100	100
17	21	157/159 (99%)	152 (97%)	5 (3%)	0	100	100
18	22	97/99 (98%)	94 (97%)	3 (3%)	0	100	100
19	cc	116/118 (98%)	114 (98%)	2 (2%)	0	100	100
20	26	132/134 (98%)	132 (100%)	0	0	100	100
21	27	133/135 (98%)	127 (96%)	6 (4%)	0	100	100
22	dd	145/147 (99%)	139 (96%)	6 (4%)	0	100	100
23	29	100/245 (41%)	97 (97%)	3 (3%)	0	100	100
24	31	105/107 (98%)	101 (96%)	4 (4%)	0	100	100
25	32	126/128 (98%)	124 (98%)	2 (2%)	0	100	100
26	ee	107/109 (98%)	106 (99%)	1 (1%)	0	100	100
27	34	112/114 (98%)	112 (100%)	0	0	100	100
28	35	120/122 (98%)	117 (98%)	2 (2%)	1 (1%)	16	25
29	36	100/102 (98%)	99 (99%)	1 (1%)	0	100	100
30	37	84/86 (98%)	84 (100%)	0	0	100	100
31	38	67/69 (97%)	66 (98%)	1 (2%)	0	100	100
32	39	48/50 (96%)	48 (100%)	0	0	100	100
33	40	50/52 (96%)	50 (100%)	0	0	100	100
34	41	23/25 (92%)	23 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
35	42	102/104 (98%)	100 (98%)	2 (2%)	0	100	100
36	ff	89/91 (98%)	85 (96%)	4 (4%)	0	100	100
37	gg	122/124 (98%)	120 (98%)	2 (2%)	0	100	100
38	s	194/196 (99%)	187 (96%)	7 (4%)	0	100	100
39	EB	373/375 (100%)	361 (97%)	12 (3%)	0	100	100
40	Q	185/188 (98%)	180 (97%)	5 (3%)	0	100	100
41	10	205/213 (96%)	200 (98%)	5 (2%)	0	100	100
42	L9	188/190 (99%)	181 (96%)	7 (4%)	0	100	100
43	S7	181/189 (96%)	178 (98%)	3 (2%)	0	100	100
44	S9	183/185 (99%)	181 (99%)	2 (1%)	0	100	100
45	S4	260/262 (99%)	257 (99%)	3 (1%)	0	100	100
46	S6	235/237 (99%)	235 (100%)	0	0	100	100
47	SS	122/124 (98%)	121 (99%)	1 (1%)	0	100	100
48	RR	139/141 (99%)	134 (96%)	4 (3%)	1 (1%)	18	28
49	YY	53/55 (96%)	53 (100%)	0	0	100	100
50	LL	142/144 (99%)	137 (96%)	5 (4%)	0	100	100
51	11	168/170 (99%)	165 (98%)	3 (2%)	0	100	100
52	GG	133/135 (98%)	132 (99%)	1 (1%)	0	100	100
53	23	137/139 (99%)	135 (98%)	2 (2%)	0	100	100
54	19	178/180 (99%)	176 (99%)	2 (1%)	0	100	100
55	v	842/857 (98%)	832 (99%)	10 (1%)	0	100	100
56	S3	226/228 (99%)	223 (99%)	3 (1%)	0	100	100
57	FF	147/149 (99%)	145 (99%)	2 (1%)	0	100	100
58	S8	204/206 (99%)	200 (98%)	4 (2%)	0	100	100
59	S2	219/221 (99%)	214 (98%)	5 (2%)	0	100	100
60	BB	215/295 (73%)	210 (98%)	5 (2%)	0	100	100
61	UU	99/101 (98%)	97 (98%)	2 (2%)	0	100	100
62	PP	81/83 (98%)	78 (96%)	3 (4%)	0	100	100
63	JJ	130/132 (98%)	127 (98%)	3 (2%)	0	100	100
64	AS	211/213 (99%)	205 (97%)	6 (3%)	0	100	100
65	VV	81/83 (98%)	80 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
66	QQ	127/129 (98%)	124 (98%)	3 (2%)	0	100	100
67	24	96/157 (61%)	95 (99%)	1 (1%)	0	100	100
68	30	112/114 (98%)	108 (96%)	3 (3%)	1 (1%)	14	22
69	ZZ	66/68 (97%)	64 (97%)	2 (3%)	0	100	100
71	MM	139/141 (99%)	136 (98%)	3 (2%)	0	100	100
72	AA	311/313 (99%)	297 (96%)	14 (4%)	0	100	100
73	OO	98/100 (98%)	97 (99%)	1 (1%)	0	100	100
74	RB	54/407 (13%)	52 (96%)	2 (4%)	0	100	100
75	EE	115/132 (87%)	113 (98%)	2 (2%)	0	100	100
76	CC	94/96 (98%)	90 (96%)	3 (3%)	1 (1%)	11	18
77	II	140/142 (99%)	137 (98%)	3 (2%)	0	100	100
78	TT	73/75 (97%)	72 (99%)	1 (1%)	0	100	100
79	WW	60/62 (97%)	59 (98%)	1 (2%)	0	100	100
80	XX	53/55 (96%)	52 (98%)	1 (2%)	0	100	100
81	B	146/149 (98%)	142 (97%)	3 (2%)	1 (1%)	18	28
82	u	215/217 (99%)	210 (98%)	5 (2%)	0	100	100
83	S5	181/191 (95%)	176 (97%)	4 (2%)	1 (1%)	21	32
84	A	129/131 (98%)	121 (94%)	8 (6%)	0	100	100
85	t	151/153 (99%)	139 (92%)	11 (7%)	1 (1%)	18	28
All	All	13211/14215 (93%)	12903 (98%)	297 (2%)	11 (0%)	49	64

5 of 11 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	17	169	LYS
12	13	47	ALA
48	RR	62	PRO
81	B	51	HIS
5	L8	14	SER

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	17	162/162 (100%)	153 (94%)	9 (6%)	19	33
2	DD	130/136 (96%)	127 (98%)	3 (2%)	44	66
5	L8	190/190 (100%)	179 (94%)	11 (6%)	18	32
6	L3	342/342 (100%)	321 (94%)	21 (6%)	17	30
7	L4	302/302 (100%)	293 (97%)	9 (3%)	36	58
8	L5	247/247 (100%)	239 (97%)	8 (3%)	34	56
9	L6	190/251 (76%)	182 (96%)	8 (4%)	26	45
10	L7	196/220 (89%)	191 (97%)	5 (3%)	40	63
11	aa	200/205 (98%)	189 (94%)	11 (6%)	19	34
12	13	175/198 (88%)	168 (96%)	7 (4%)	28	47
13	14	117/117 (100%)	113 (97%)	4 (3%)	32	54
14	15	171/171 (100%)	162 (95%)	9 (5%)	20	36
15	bb	171/171 (100%)	165 (96%)	6 (4%)	32	53
16	20	157/157 (100%)	145 (92%)	12 (8%)	12	21
17	21	139/139 (100%)	133 (96%)	6 (4%)	26	44
18	22	89/89 (100%)	84 (94%)	5 (6%)	19	33
19	cc	106/106 (100%)	101 (95%)	5 (5%)	23	41
20	26	124/124 (100%)	114 (92%)	10 (8%)	11	18
21	27	117/117 (100%)	111 (95%)	6 (5%)	21	37
22	dd	119/119 (100%)	115 (97%)	4 (3%)	32	54
23	29	84/184 (46%)	82 (98%)	2 (2%)	43	65
24	31	98/98 (100%)	89 (91%)	9 (9%)	8	14
25	32	114/114 (100%)	111 (97%)	3 (3%)	40	63
26	ee	88/88 (100%)	81 (92%)	7 (8%)	11	19
27	34	98/98 (100%)	95 (97%)	3 (3%)	35	57
28	35	109/109 (100%)	105 (96%)	4 (4%)	30	51
29	36	86/86 (100%)	83 (96%)	3 (4%)	32	53
30	37	73/73 (100%)	71 (97%)	2 (3%)	39	62
31	38	64/64 (100%)	59 (92%)	5 (8%)	11	20
32	39	47/47 (100%)	47 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
33	40	48/48 (100%)	47 (98%)	1 (2%)	47	69
34	41	24/24 (100%)	24 (100%)	0	100	100
35	42	92/92 (100%)	87 (95%)	5 (5%)	20	35
36	ff	74/74 (100%)	70 (95%)	4 (5%)	20	35
37	gg	107/108 (99%)	103 (96%)	4 (4%)	30	51
38	s	164/164 (100%)	155 (94%)	9 (6%)	19	34
39	EB	321/321 (100%)	310 (97%)	11 (3%)	32	54
40	Q	164/165 (99%)	157 (96%)	7 (4%)	26	44
41	10	178/180 (99%)	167 (94%)	11 (6%)	16	29
42	L9	169/169 (100%)	153 (90%)	16 (10%)	8	13
43	S7	165/169 (98%)	160 (97%)	5 (3%)	36	58
44	S9	161/161 (100%)	157 (98%)	4 (2%)	42	64
45	S4	224/224 (100%)	220 (98%)	4 (2%)	51	73
46	S6	207/207 (100%)	205 (99%)	2 (1%)	68	84
47	SS	107/107 (100%)	103 (96%)	4 (4%)	30	51
48	RR	113/113 (100%)	111 (98%)	2 (2%)	51	73
49	YY	46/46 (100%)	46 (100%)	0	100	100
50	LL	125/125 (100%)	120 (96%)	5 (4%)	28	47
51	11	143/143 (100%)	136 (95%)	7 (5%)	22	39
52	GG	105/105 (100%)	98 (93%)	7 (7%)	15	26
53	23	106/106 (100%)	105 (99%)	1 (1%)	70	85
54	19	159/159 (100%)	153 (96%)	6 (4%)	29	49
55	v	723/728 (99%)	700 (97%)	23 (3%)	34	56
56	S3	190/190 (100%)	177 (93%)	13 (7%)	14	25
57	FF	130/130 (100%)	126 (97%)	4 (3%)	35	57
58	S8	178/178 (100%)	171 (96%)	7 (4%)	28	48
59	S2	187/187 (100%)	178 (95%)	9 (5%)	23	40
60	BB	180/244 (74%)	174 (97%)	6 (3%)	33	55
61	UU	88/88 (100%)	84 (96%)	4 (4%)	24	42
62	PP	67/67 (100%)	62 (92%)	5 (8%)	12	21
63	JJ	119/119 (100%)	114 (96%)	5 (4%)	26	45

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
64	AS	194/194 (100%)	187 (96%)	7 (4%)	31	52
65	VV	75/75 (100%)	74 (99%)	1 (1%)	61	80
66	QQ	112/112 (100%)	111 (99%)	1 (1%)	70	85
67	24	82/126 (65%)	81 (99%)	1 (1%)	63	81
68	30	97/97 (100%)	93 (96%)	4 (4%)	27	46
69	ZZ	61/61 (100%)	56 (92%)	5 (8%)	10	18
71	MM	111/111 (100%)	108 (97%)	3 (3%)	39	62
72	AA	272/272 (100%)	264 (97%)	8 (3%)	37	60
73	OO	92/92 (100%)	86 (94%)	6 (6%)	15	27
74	RB	47/326 (14%)	46 (98%)	1 (2%)	47	69
75	EE	99/108 (92%)	96 (97%)	3 (3%)	36	58
76	CC	87/87 (100%)	81 (93%)	6 (7%)	14	24
77	II	117/117 (100%)	113 (97%)	4 (3%)	32	54
78	TT	66/66 (100%)	65 (98%)	1 (2%)	57	77
79	WW	55/55 (100%)	53 (96%)	2 (4%)	31	52
80	XX	48/48 (100%)	47 (98%)	1 (2%)	47	69
81	B	123/123 (100%)	122 (99%)	1 (1%)	73	86
82	u	196/196 (100%)	194 (99%)	2 (1%)	68	84
83	S5	158/161 (98%)	154 (98%)	4 (2%)	42	64
84	A	117/117 (100%)	107 (92%)	10 (8%)	10	16
85	t	126/126 (100%)	116 (92%)	10 (8%)	11	19
All	All	11504/12135 (95%)	11035 (96%)	469 (4%)	28	46

5 of 469 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
40	Q	31	LEU
82	u	41	TYR
50	LL	9	PHE
78	TT	90	GLU
68	30	57	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 145 such sidechains are listed below:

Mol	Chain	Res	Type
58	S8	167	GLN
82	u	143	ASN
63	JJ	121	GLN
72	AA	237	ASN
22	dd	66	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
3	58	149/156 (95%)	24 (16%)	1 (0%)
4	5	119/120 (99%)	8 (6%)	0
70	18	1652/1698 (97%)	335 (20%)	16 (0%)
86	28	3473/4807 (72%)	634 (18%)	46 (1%)
87	ES	34/5070 (0%)	7 (20%)	1 (2%)
All	All	5427/11851 (45%)	1008 (18%)	64 (1%)

5 of 1008 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
3	58	2	G
3	58	23	C
3	58	34	U
3	58	35	C
3	58	39	G

5 of 64 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
86	28	4719	G
86	28	4898	G
86	28	485	C
86	28	480	C
86	28	4925	U

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

2 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond

length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
55	DDE	v	715	55	18,20,21	1.04	1 (5%)	17,28,30	1.36	2 (11%)
81	5CT	B	50	81	13,14,15	0.63	0	8,15,17	0.60	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
55	DDE	v	715	55	-	6/20/21/23	0/1/1/1
81	5CT	B	50	81	-	7/13/14/16	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
55	v	715	DDE	CD2-CG	2.37	1.41	1.36

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
55	v	715	DDE	CA-CB-CG	-3.24	105.78	113.77
55	v	715	DDE	CB-CG-CD2	-3.13	122.94	129.33

There are no chirality outliers.

5 of 13 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
55	v	715	DDE	C-CA-CB-CG
55	v	715	DDE	NAD-CBI-CBW-NCB
81	B	50	5CT	NZ-C1-C2-C3
81	B	50	5CT	NZ-C1-C2-O1
81	B	50	5CT	O1-C2-C3-C4

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
55	v	715	DDE	1	0
81	B	50	5CT	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 5 are monoatomic - leaving 1 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
89	GDP	v	900	-	29,30,30	3.43	13 (44%)	45,47,47	1.87	13 (28%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
89	GDP	v	900	-	-	3/16/32/32	0/3/3/3

The worst 5 of 13 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
89	v	900	GDP	O6-C6	9.49	1.41	1.23
89	v	900	GDP	C2'-C3'	-7.93	1.31	1.53
89	v	900	GDP	O4'-C4'	-6.52	1.30	1.45
89	v	900	GDP	O4'-C1'	5.46	1.54	1.42
89	v	900	GDP	C2-N2	4.57	1.44	1.34

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
89	v	900	GDP	C5-C4-N3	-5.87	119.05	128.39
89	v	900	GDP	C2-N3-C4	4.68	120.36	112.30
89	v	900	GDP	N9-C4-N3	4.14	134.22	125.95
89	v	900	GDP	C2'-C3'-C4'	3.13	108.65	102.61
89	v	900	GDP	C8-N7-C5	2.81	109.26	104.26

There are no chirality outliers.

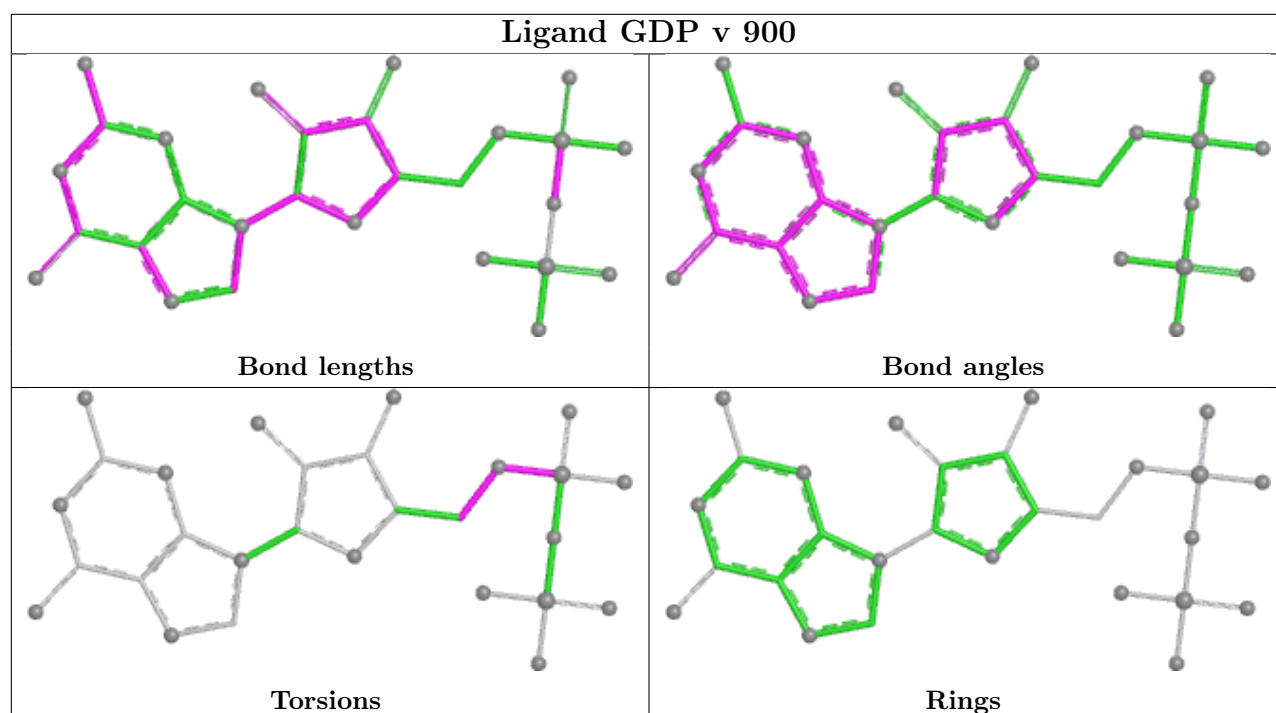
All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
89	v	900	GDP	C5'-O5'-PA-O3A
89	v	900	GDP	C5'-O5'-PA-O2A
89	v	900	GDP	C4'-C5'-O5'-PA

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
70	18	5
74	RB	1

The worst 5 of 6 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	RB	225:LEU	C	282:THR	N	56.11
1	18	834:C	O3'	841:G	P	17.67
1	18	1417:C	O3'	1423:C	P	17.04
1	18	745:C	O3'	749:U	P	7.75
1	18	225:G	O3'	287:U	P	4.54

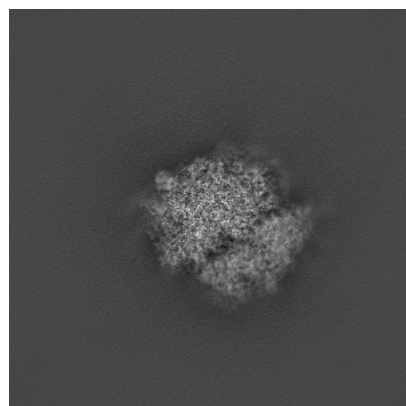
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-75724. These allow visual inspection of the internal detail of the map and identification of artifacts.

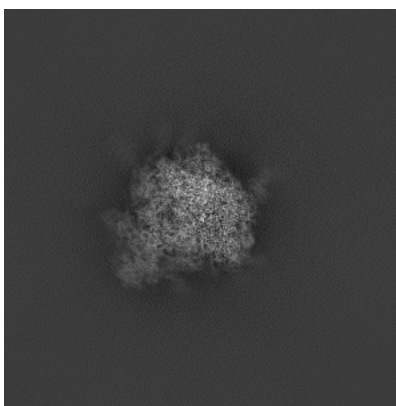
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

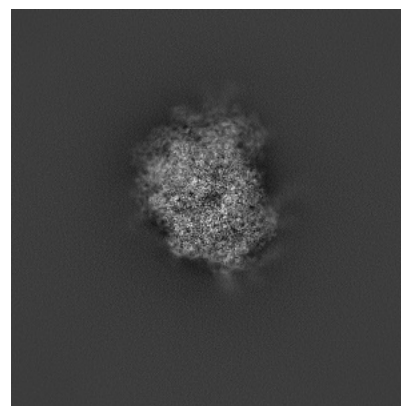
6.1.1 Primary map



X

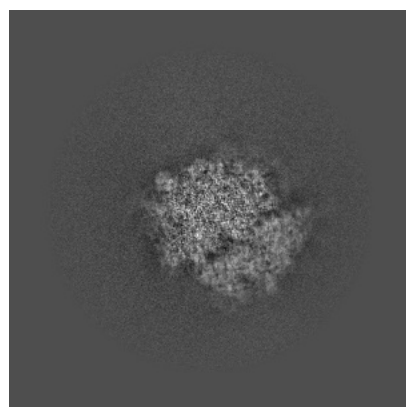


Y

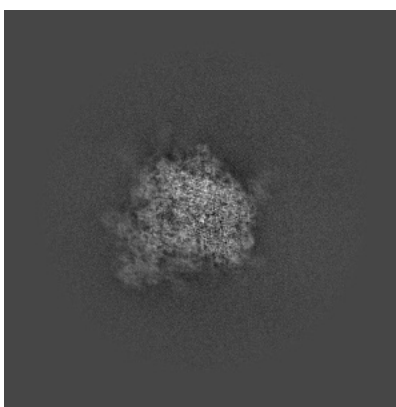


Z

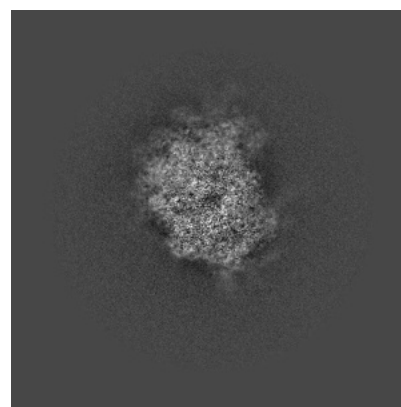
6.1.2 Raw map



X



Y

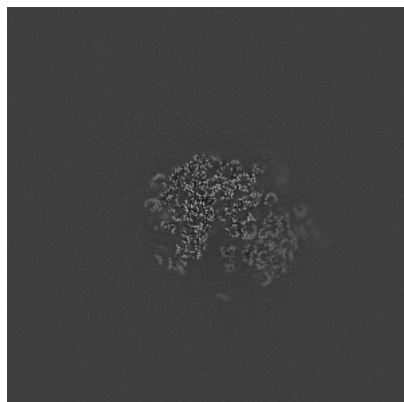


Z

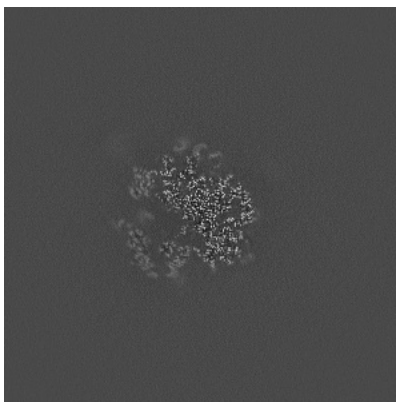
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

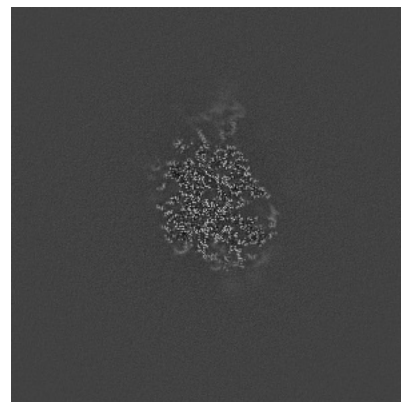
6.2.1 Primary map



X Index: 400

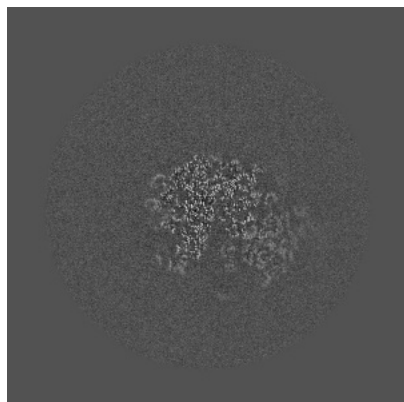


Y Index: 400

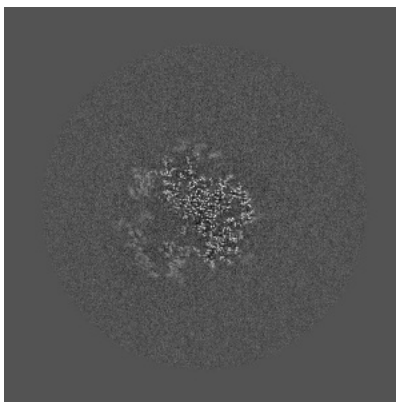


Z Index: 400

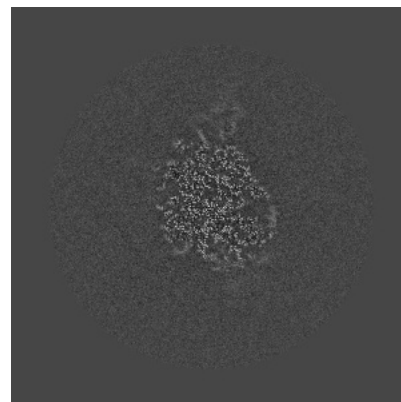
6.2.2 Raw map



X Index: 400



Y Index: 400

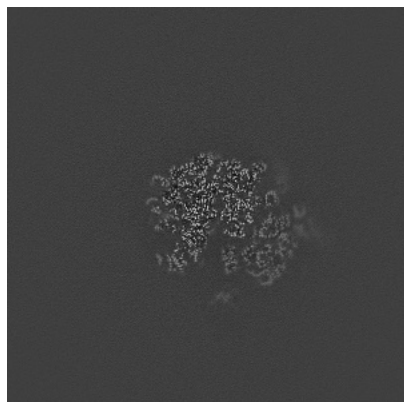


Z Index: 400

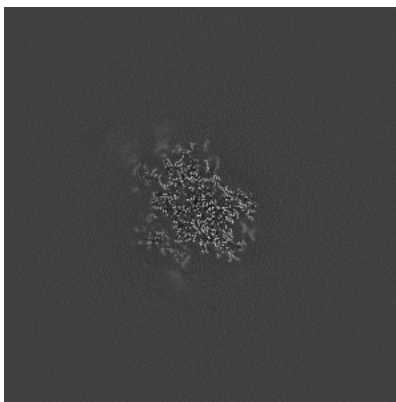
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

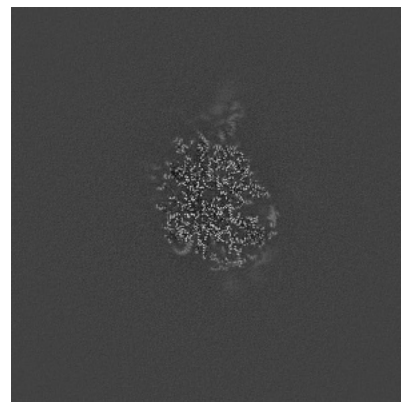
6.3.1 Primary map



X Index: 396

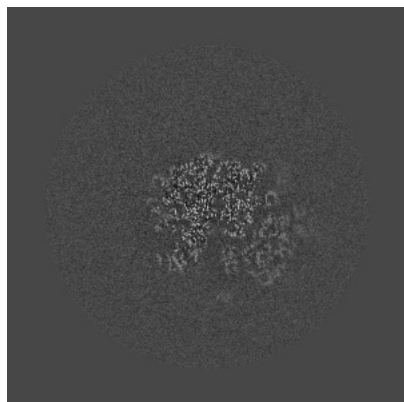


Y Index: 380

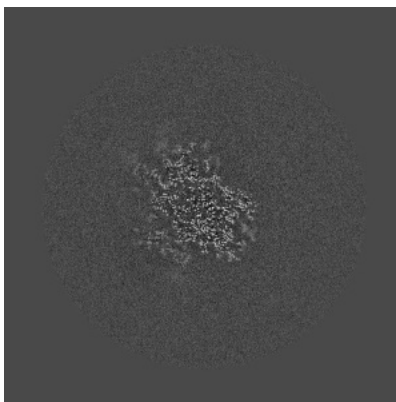


Z Index: 402

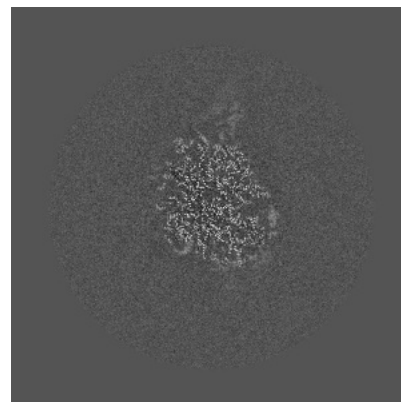
6.3.2 Raw map



X Index: 396



Y Index: 380

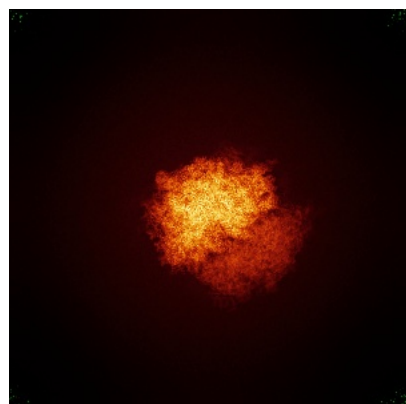


Z Index: 402

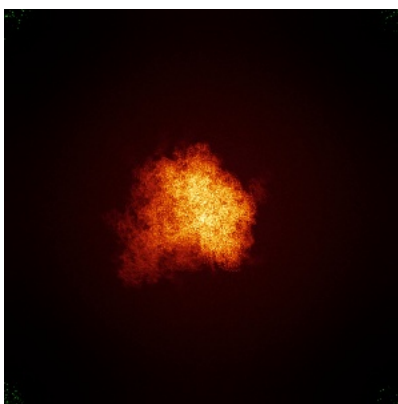
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

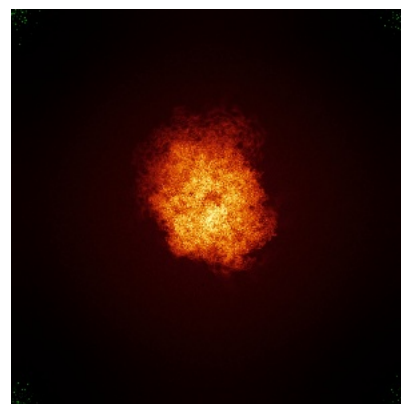
6.4.1 Primary map



X

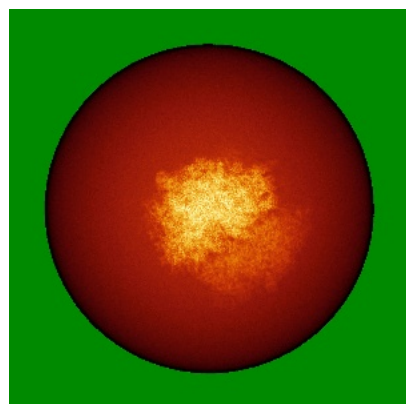


Y

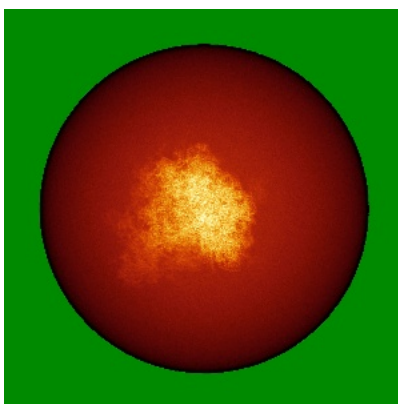


Z

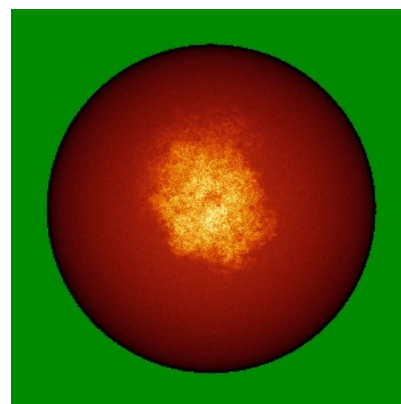
6.4.2 Raw map



X



Y



Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

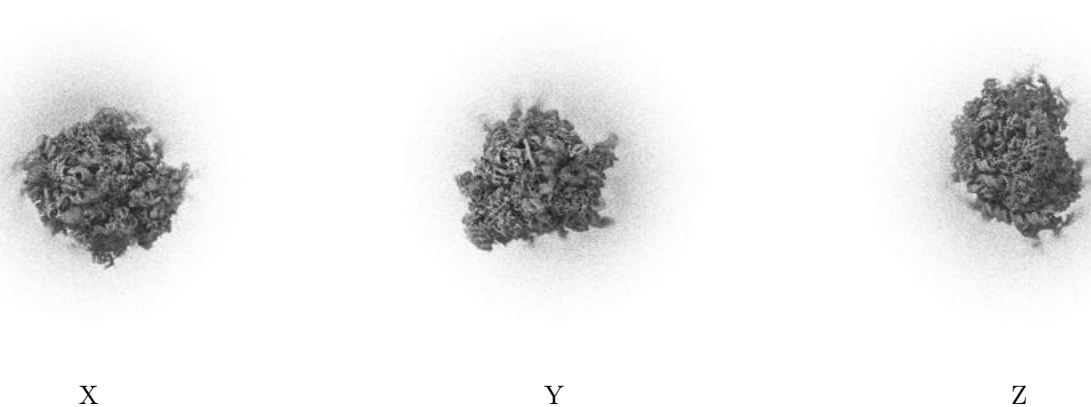
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 2.4. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

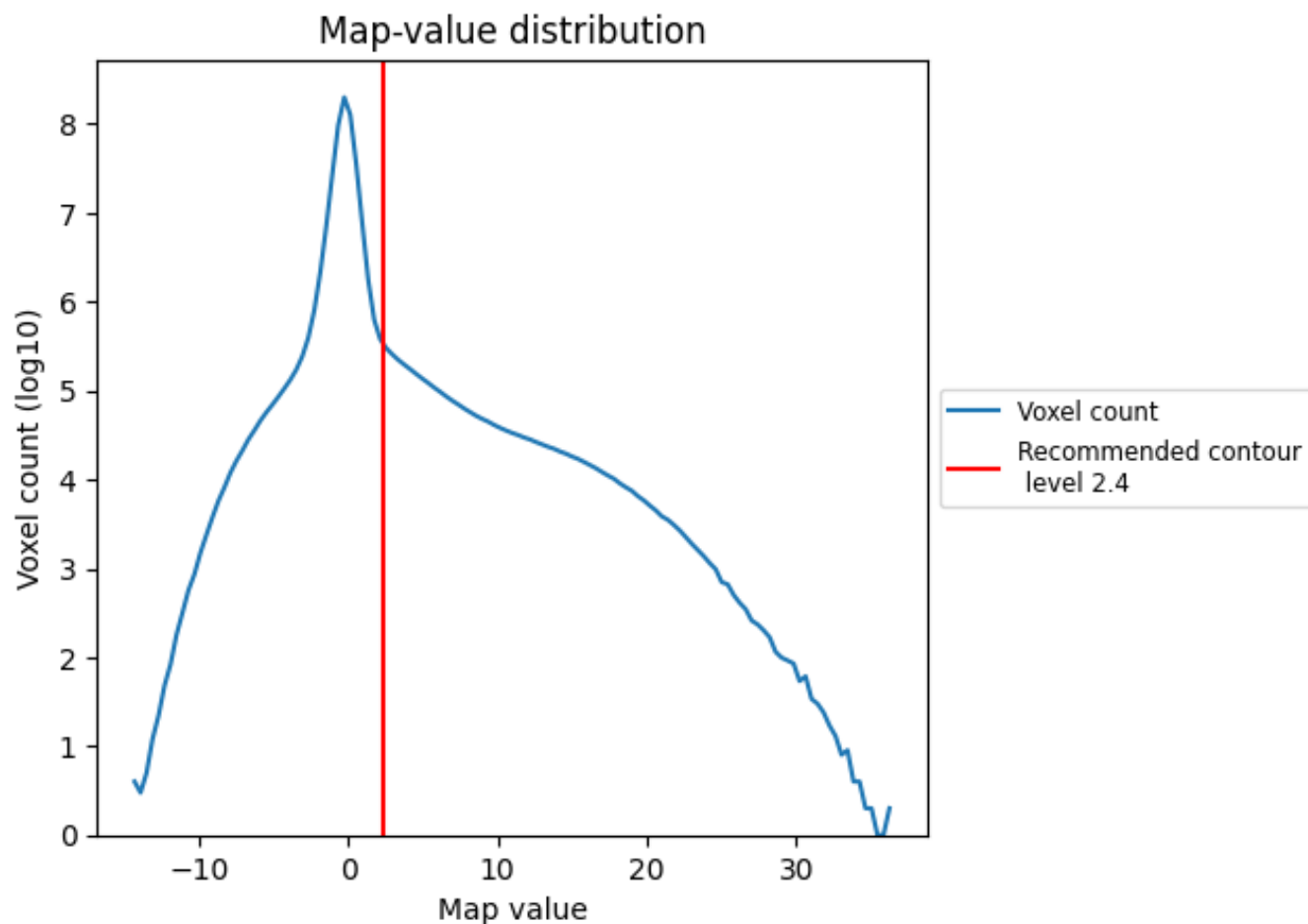
6.6 Mask visualisation [i](#)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis [i](#)

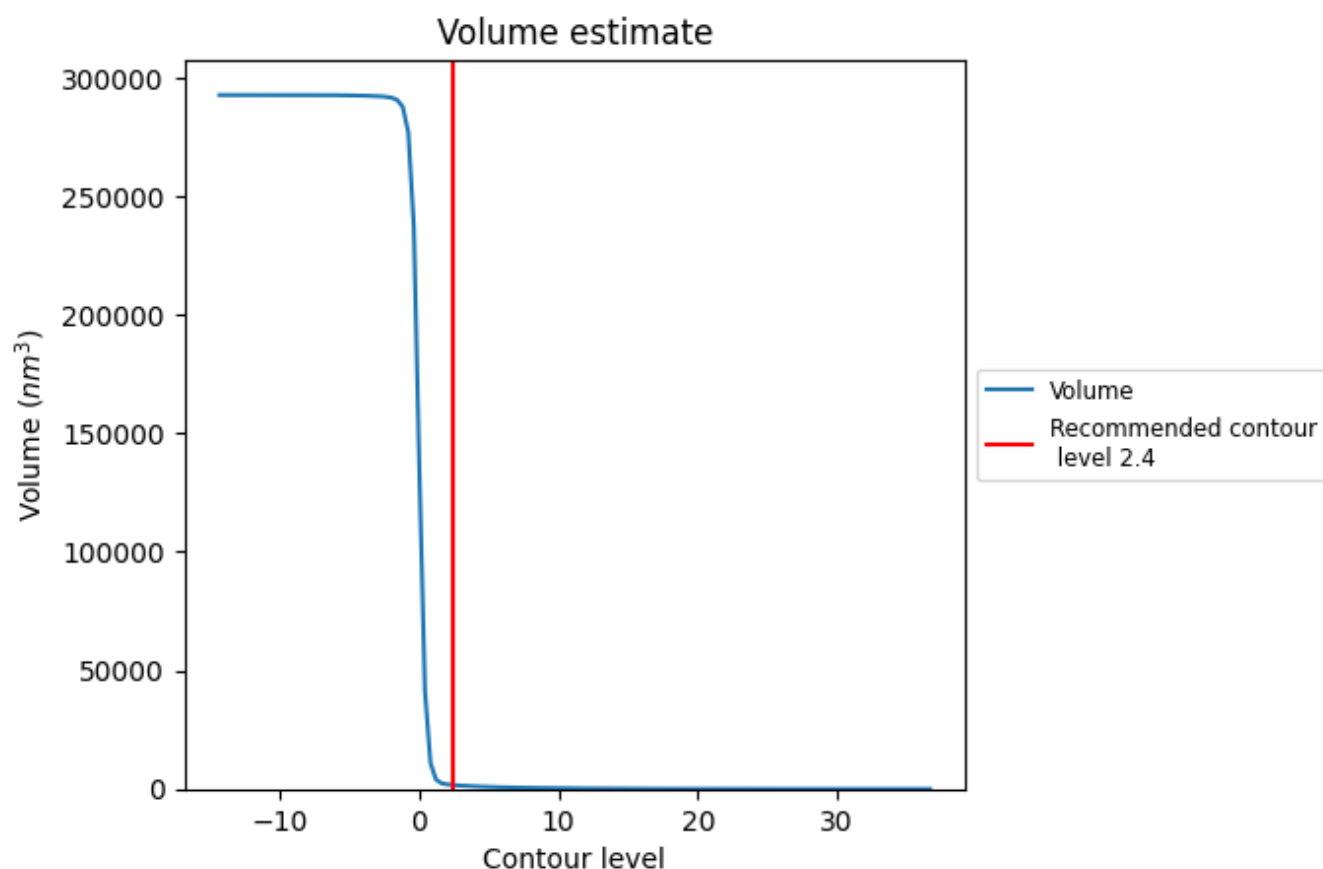
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

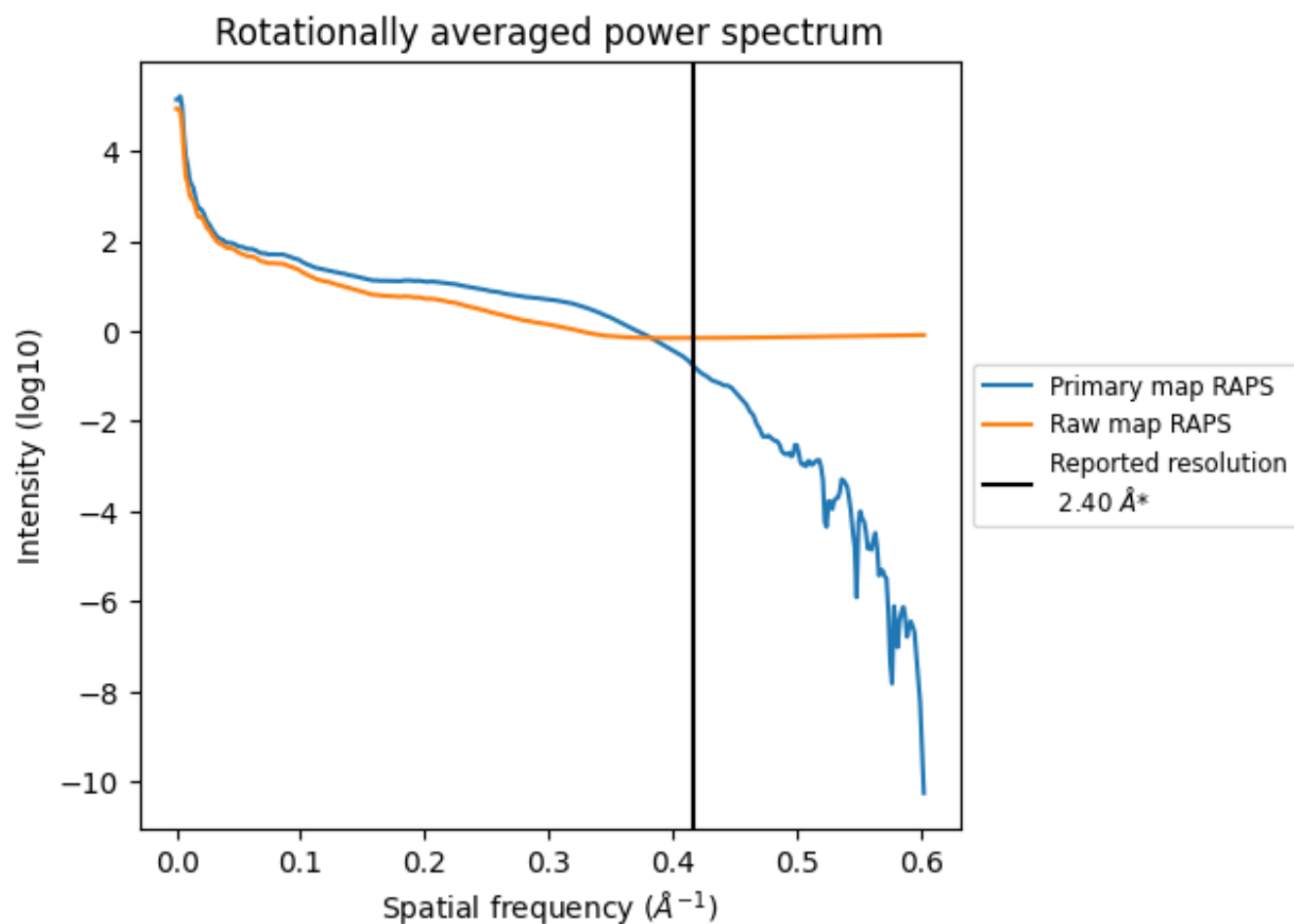
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1691 nm^3 ; this corresponds to an approximate mass of 1528 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

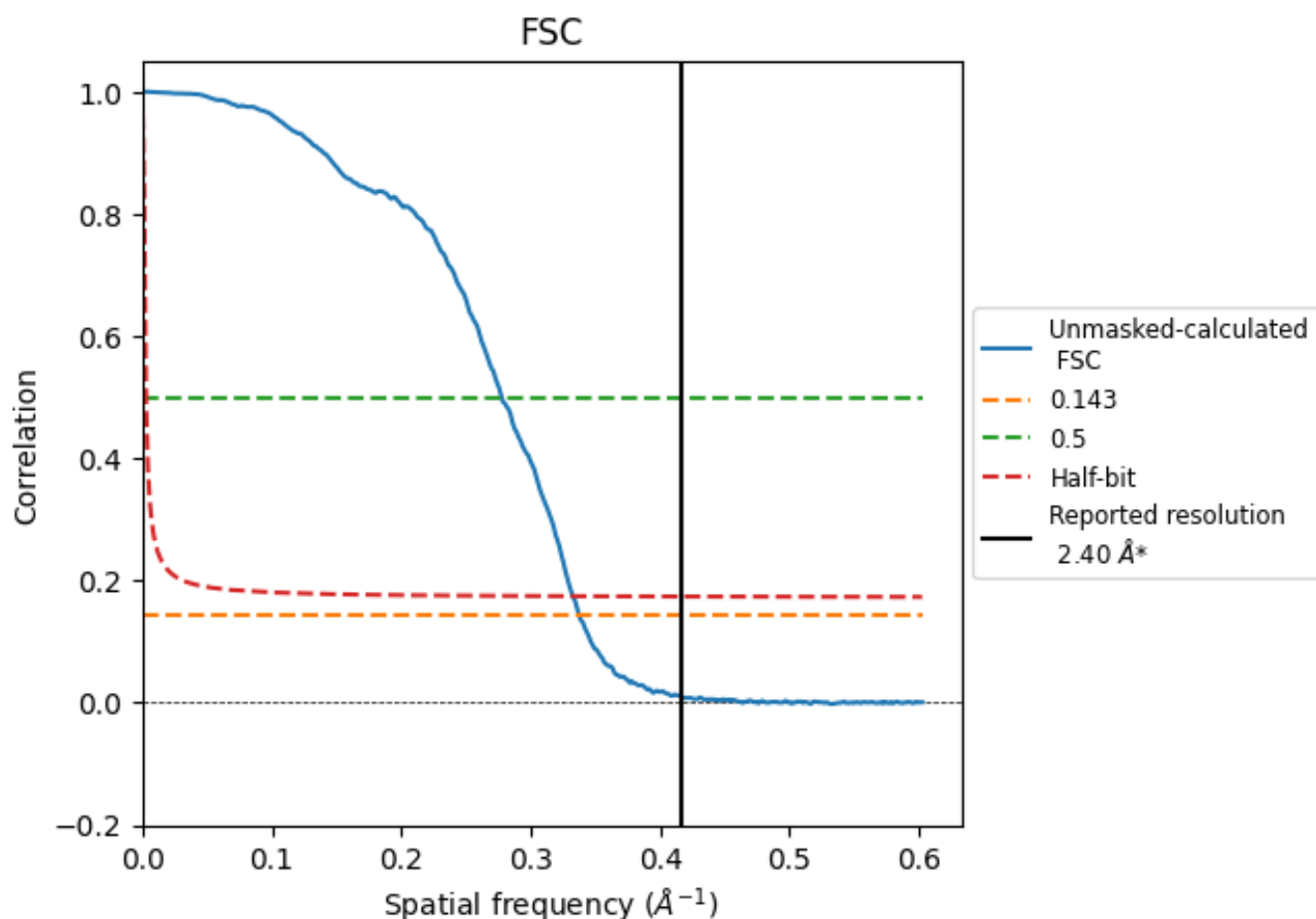


*Reported resolution corresponds to spatial frequency of 0.417 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.417 Å⁻¹

8.2 Resolution estimates [i](#)

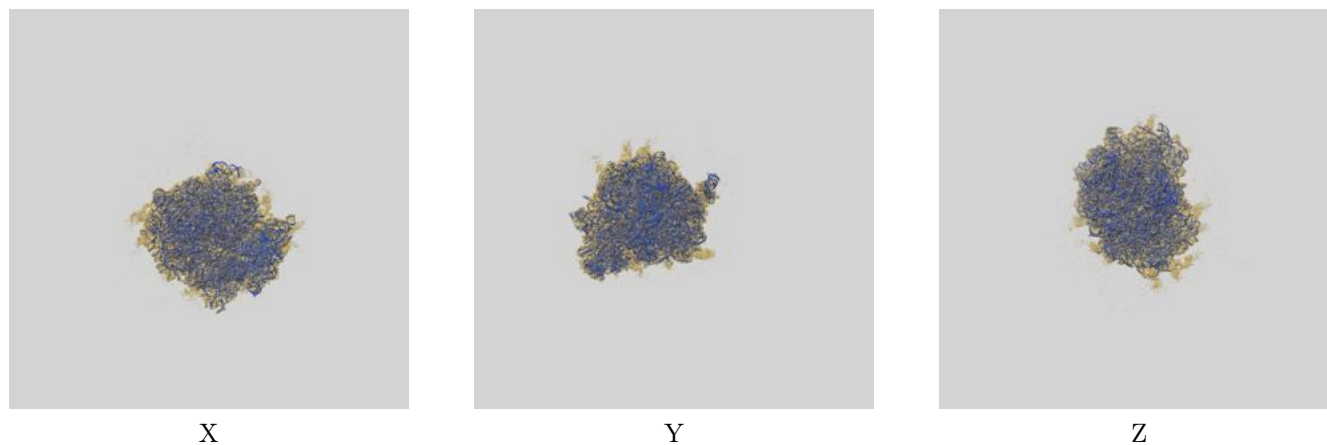
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.40	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	2.96	3.60	3.01

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 2.96 differs from the reported value 2.4 by more than 10 %

9 Map-model fit [i](#)

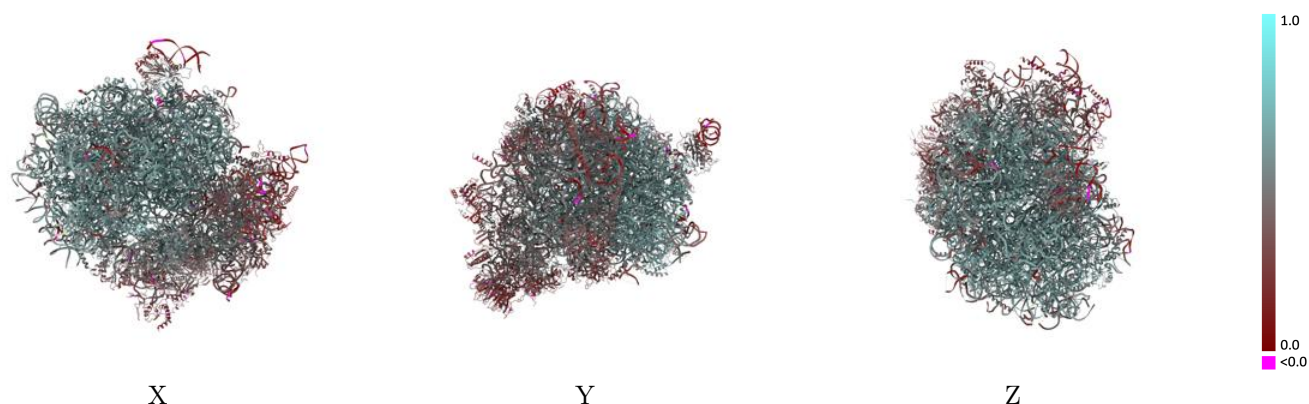
This section contains information regarding the fit between EMDB map EMD-75724 and PDB model 1IQ. Per-residue inclusion information can be found in section 3 on page 21.

9.1 Map-model overlay [i](#)



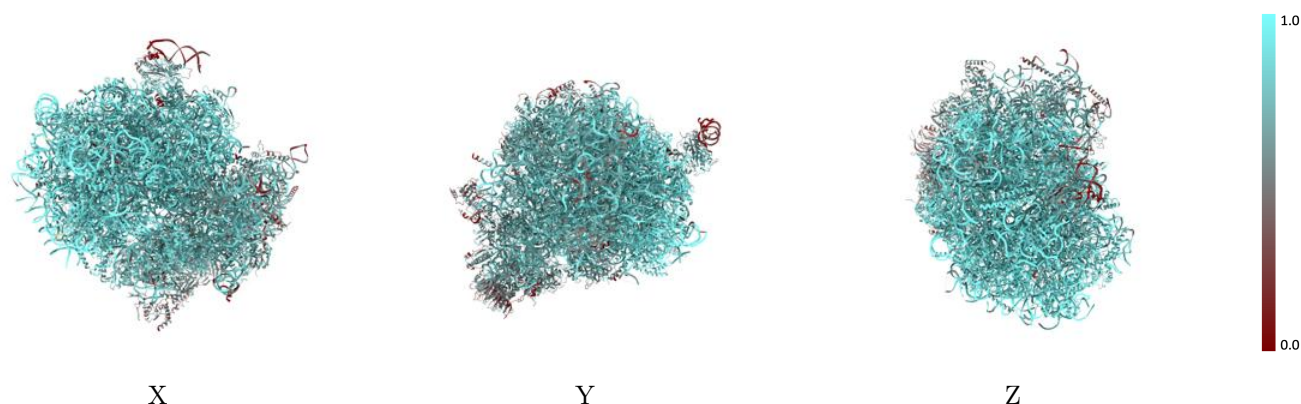
The images above show the 3D surface view of the map at the recommended contour level 2.4 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



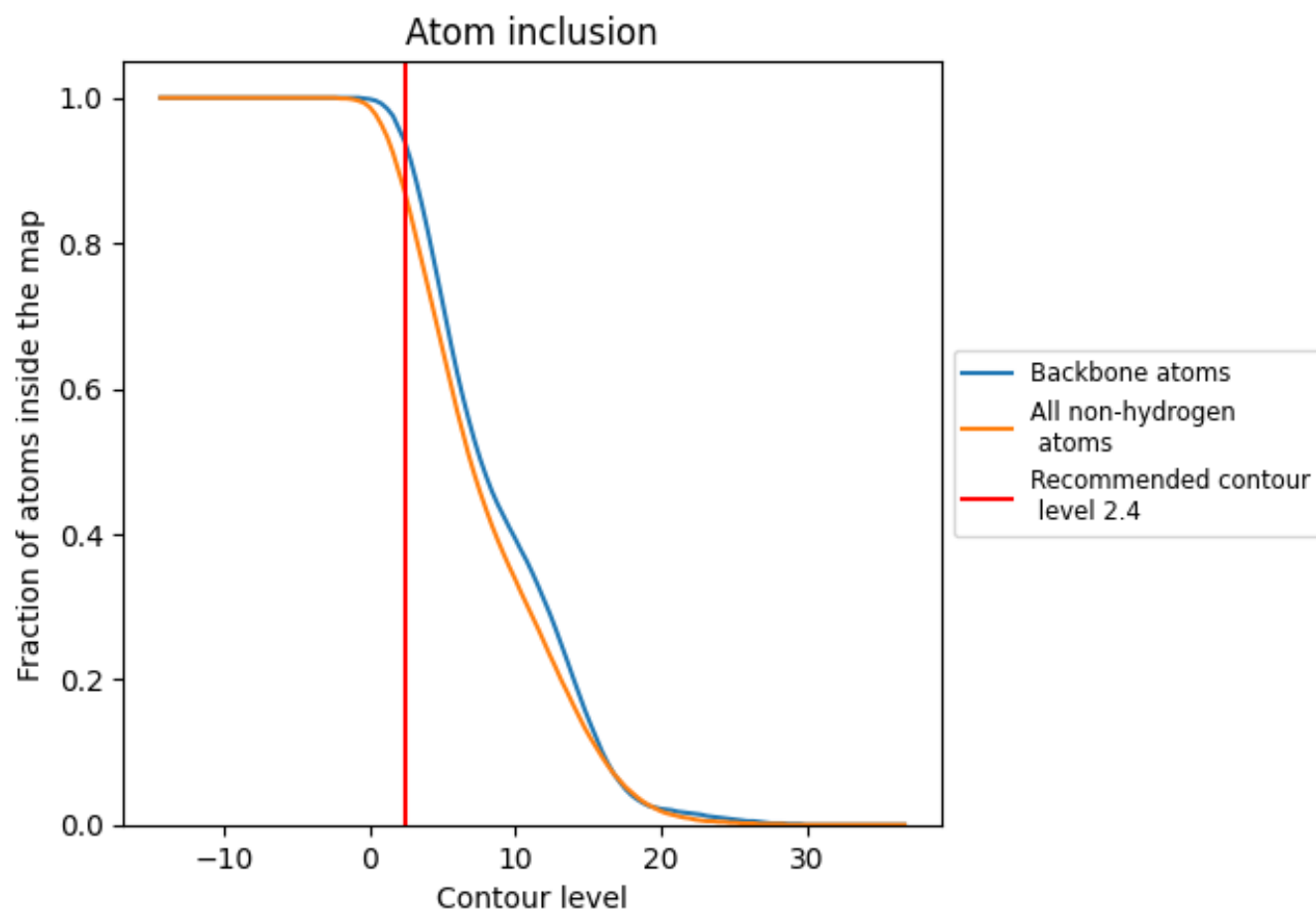
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (2.4).

9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 87% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (2.4) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8720	 0.5110
10	 0.9180	 0.5890
11	 0.8760	 0.5400
13	 0.9160	 0.5800
14	 0.9250	 0.5780
15	 0.9670	 0.6280
17	 0.7970	 0.5300
18	 0.8800	 0.4320
19	 0.8880	 0.5520
20	 0.9450	 0.6080
21	 0.9290	 0.5850
22	 0.8550	 0.4890
23	 0.9380	 0.6110
24	 0.7360	 0.4660
26	 0.9260	 0.5880
27	 0.9360	 0.5760
28	 0.9690	 0.5770
29	 0.8550	 0.5300
30	 0.8420	 0.5480
31	 0.9090	 0.5660
32	 0.9620	 0.6210
34	 0.9290	 0.5980
35	 0.9190	 0.5820
36	 0.9110	 0.5640
37	 0.9610	 0.6210
38	 0.8400	 0.5330
39	 0.9420	 0.5900
40	 0.9160	 0.5920
41	 0.8390	 0.5300
42	 0.9300	 0.5940
5	 0.9930	 0.6090
58	 0.9750	 0.5890
A	 0.7070	 0.3690
AA	 0.4480	 0.2470
AS	 0.6890	 0.3760



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Chain	Atom inclusion	Q-score
B	 0.8300	 0.5520
BB	 0.6870	 0.4170
CC	 0.6580	 0.3430
DD	 0.7460	 0.4530
EB	 0.6630	 0.4040
EE	 0.4070	 0.2070
ES	 0.1730	 0.1100
FF	 0.7530	 0.4440
GG	 0.6930	 0.3770
II	 0.5930	 0.3330
JJ	 0.5990	 0.3390
L3	 0.9470	 0.6080
L4	 0.9570	 0.6070
L5	 0.9280	 0.5740
L6	 0.9310	 0.5720
L7	 0.9530	 0.6170
L8	 0.9590	 0.6190
L9	 0.9110	 0.5790
LL	 0.6930	 0.3640
MM	 0.6500	 0.3310
OO	 0.5790	 0.3130
PP	 0.7150	 0.4250
Q	 0.9570	 0.6170
QQ	 0.7840	 0.4970
RB	 0.5750	 0.3830
RR	 0.8280	 0.5270
S2	 0.7430	 0.4510
S3	 0.6570	 0.3870
S4	 0.6860	 0.4020
S5	 0.6400	 0.3600
S6	 0.5740	 0.2740
S7	 0.6070	 0.3500
S8	 0.6720	 0.3680
S9	 0.7220	 0.4170
SS	 0.6130	 0.3270
TT	 0.5880	 0.3030
UU	 0.7310	 0.4310
VV	 0.6900	 0.3950
WW	 0.6000	 0.3200
XX	 0.7510	 0.4190
YY	 0.6500	 0.3840
ZZ	 0.5490	 0.2780

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Chain	Atom inclusion	Q-score
aa	 0.8950	 0.5560
bb	 0.9550	 0.6100
cc	 0.9150	 0.5870
dd	 0.9560	 0.6220
ee	 0.9640	 0.6270
ff	 0.9260	 0.5940
gg	 0.9560	 0.6050
s	 0.7600	 0.4210
t	 0.5610	 0.2810
u	 0.7600	 0.4740
v	 0.8020	 0.4950